

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2000, 18:27:02 ; Search time 1381.26 Seconds
(without alignments)
-3066.588 Million cell updates/sec

Title: US-09-388-090-3
Perfect score: 1395
Sequence: 1 gtttcaaaaataccaata.....tcaggcgcaagtccccgtcaa 1395

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0
Searched: 821193 seqs, -1518192014 residues

Word size : 0
Total number of hits satisfying chosen parameters: 1642386

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Listing first 1000 summaries

Database :

GenEmbl.*

- 1: gb_ba1.*
- 2: gb_ba2.*
- 3: gb_on.*
- 4: gb_ov.*
- 5: gb_pat.*
- 6: gb_ph.*
- 7: gb_p11.*
- 8: gb_p12.*
- 9: gb_p13.*
- 10: gb_pr2.*
- 11: gb_pr3.*
- 12: gb_ro.*
- 13: gb_sts.*
- 14: gb_sy.*
- 15: gb_un.*
- 16: gb_vi.*
- 17: em_fun.*
- 18: em_hum1.*
- 19: em_hum2.*
- 20: em_in.*
- 21: em_om.*
- 22: em_or.*
- 23: em_ov.*
- 24: em_pat.*
- 25: em_ph.*
- 26: em_pl.*
- 27: em_ro.*
- 28: em_sts.*
- 29: em_sy.*
- 30: em_un.*
- 31: em_vi.*
- 32: gb_htg1.*
- 33: gb_htg2.*
- 34: gb_in1.*
- 35: gb_in2.*
- 36: gb_ba1.*
- 37: gb_ba2.*
- 38: em_hum3.*
- 39: em_hum4.*
- 40: gb_pr4.*
- 41: gb_htg3.*
- 42: gb_htg4.*
- 43: gb_htg5.*

- 44: gb_htg6.*
- 45: gb_htg7.*
- 46: em_htg1.*
- 47: em_htg2.*
- 48: em_htg3.*
- 49: em_hum5.*
- 50: gb_p13.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
C 1	23	1.6	91	34	AG2H417
C 2	23	1.6	93	34	AG2H442
C 3	20	1.4	1435	4	GGU72352
C 4	20	1.4	2890	1	GOGDH
C 5	20	1.4	31427	43	AC013843
C 6	20	1.4	144734	33	AC005052
C 7	19	1.4	2153	10	HTLV1RES
C 8	19	1.4	4316	2	AF072440
C 9	19	1.4	6417	12	AF067430
C 10	19	1.4	36679	34	CEL14F9
C 11	19	1.4	38012	8	SPC2F12
C 12	19	1.4	60476	7	AB016875
C 13	19	1.4	93419	32	AC002415
C 14	18	1.3	247	12	MUSTHREX17
C 15	18	1.3	400	13	GI4673
C 16	18	1.3	423	1	AB011872
C 17	18	1.3	459	9	HSGATA3P
C 18	18	1.3	559	16	HSVR3AN
C 19	18	1.3	1474	34	GI083277
C 20	18	1.3	1549	7	D78602
C 21	18	1.3	1664	4	DRGROUCH1
C 22	18	1.3	1796	12	AF087654
C 23	18	1.3	1861	35	TCU14732
C 24	18	1.3	2543	35	AF188715
C 25	18	1.3	2809	10	HSU67369
C 26	18	1.3	3537	4	CHKTH8A
C 27	18	1.3	4339	12	MUSTSPLA
C 28	18	1.3	4373	1	MISPT
C 29	18	1.3	6194	41	AC008595
C 30	18	1.3	7744	1	HIFIMGC
C 31	18	1.3	9513	1	TAA224959
C 32	18	1.3	10249	2	MTU68480
C 33	18	1.3	11684	2	AE00263
C 34	18	1.3	11904	2	PAU79580
C 35	18	1.3	12360	43	AC015011
C 36	18	1.3	15131	2	AE000729
C 37	18	1.3	16951	2	MSU46844
C 38	18	1.3	19521	1	D90811
C 39	18	1.3	28611	34	CEC02D4
C 40	18	1.3	34305	34	CEW02B12
C 41	18	1.3	34983	2	SCM11
C 42	18	1.3	37005	11	AC005239
C 43	18	1.3	37085	1	MTY13D12
C 44	18	1.3	37164	1	MSGY126
C 45	18	1.3	38017	10	AC000396
C 46	18	1.3	3951	11	AC005602
C 47	18	1.3	40075	34	CEI28D6
C 48	18	1.3	41171	1	U00010
C 49	18	1.3	44189	41	AC011540
C 50	18	1.3	45097	35	CEL0416
C 51	18	1.3	46632	41	AC009588
C 52	18	1.3	54225	46	AC006090
C 53	18	1.3	55028	40	AC016473
C 54	18	1.3	56886	44	AC016415
C 55	18	1.3	67220	45	AC017014_3
C 56	18	1.3			

Continuation (4 of

57	18	1.3	73009	8	ATAC007069	AC007069 Arabidops	c 130	17	1.2	5907	1	ECSAPABCD	X97282 E.coli sapA
58	18	1.3	74901	35	AC005474	AC005474 Drosophil	131	17	1.2	6057	1	AB014757	AB014757 Pseudomon
59	18	1.3	83859	7	AB024038	AB024038 Arabidops	c 132	17	1.2	6191	2	RP075364	U75364 Rhodospseudo
60	18	1.3	100793	11	AF070717	AF070717 Homo sapi	133	17	1.2	6597	9	HSCAN	X64228 H.sapiens c
61	18	1.3	120391	45	AC017146	AC017146 Drosophil	134	17	1.2	6642	9	HUMORF10	D14689 Human MRNA
62	18	1.3	124469	41	AC008347	AC008347 Drosophil	c 135	17	1.2	6682	2	AF1170704	AF1170704 Streptomy
63	18	1.3	129441	32	HSAC002099	AC002099 Homo sapi	c 136	17	1.2	6738	2	AF116907	AF116907 Rhodococc
64	18	1.3	132353	33	AC002355	AC002355 Homo sapi	137	17	1.2	6824	6	AF112470	AF112470 Streptoco
65	18	1.3	137658	10	HS1022J11	AL049765 Human DNA	138	17	1.2	8757	4	AB018707S4	AB018710 Gallus ga
66	18	1.3	152355	11	AC005668	AC005668 Homo sapi	139	17	1.2	10477	2	AE000227	AE000227 Escherich
67	18	1.3	156187	44	AC013593	AC013593 Homo sapi	140	17	1.2	11342	1	AF005044	AF005044 Escherich
68	18	1.3	157066	42	AC010436	AC010436 Homo sapi	141	17	1.2	11344	40	AF034611	AF034611 Homo sapi
69	18	1.3	160437	43	AC011984	AC011984 Homo sapi	c 142	17	1.2	11978	2	AE001955	AE001955 Deinococc
70	18	1.3	166942	10	HS1054A22	AL031651 Human DNA	143	17	1.2	12298	16	AF092448	AF092448 Hog chole
71	18	1.3	168571	11	CNS01DUF	AL133249 BAC sequ	144	17	1.2	12298	12	AB007544	AB007544 Mus muscu
72	18	1.3	168835	11	HS652L8	AL031734 Human DNA	145	17	1.2	12437	12	AB007544	AB007544 Mus muscu
73	18	1.3	176865	42	AC008525	AC008525 Homo sapi	146	17	1.2	12457	12	AB011543	AB011543 Mus muscu
74	18	1.3	177726	11	AC004083	AC004083 Homo sapi	147	17	1.2	12653	12	D87521	D87521 Mus musculu
75	18	1.3	178328	44	AC007299	AC007299 Drosophil	148	17	1.2	13857	2	AE000185	AE000185 Escherich
76	18	1.3	183007	35	AC007257	AC007257 Drosophil	149	17	1.2	15009	43	AC014599	AC014599 Drosophil
77	18	1.3	185116	11	AC005823	AC005823 Homo sapi	150	17	1.2	15141	16	RNPLECT	M34651 Pseudorabie
78	18	1.3	202540	11	AC002524	AC002524 Homo sapi	151	17	1.2	15231	12	RNPLECT	X59601 Rat mrna fo
79	18	1.3	210296	33	HS1057B20	AL109823 Homo sapi	152	17	1.2	16578	1	D90721	D90721 Escherichia
80	18	1.3	212118	43	AC009264	AL029264 Homo sapi	153	17	1.2	17769	1	D90767	D90767 E.coli geno
81	18	1.3	310565	32	CEY62F5	AL023633 Caenorhab	154	17	1.2	18399	41	AC010652	AC010652 Homo sapi
82	18	1.3	330250	40	AF049895	AF049895 Homo sapi	c 155	17	1.2	19196	1	D90768	D90768 E.coli geno
83	18	1.3	337565	32	CEY47D3	Z98865 Caenorhabdi	c 156	17	1.2	20252	2	AF029714	AF029714 Pseudomon
84	17	1.2	129	8	AF099426	AF099426 Zea mays	c 157	17	1.2	22449	1	SPSNBCDE	Y11548 S.pristinae
85	17	1.2	135	12	MMU133878	AJ133878 Mus muscu	c 158	17	1.2	22449	1	SPSNBCGN	X38690 S.pristinae
86	17	1.2	354	9	HS303C10	Z79883 H.sapiens c	c 159	17	1.2	24754	41	CELM08674	AC008674 Homo sapi
87	17	1.2	359	13	G45126	G45126 Z17274_1 ze	c 160	17	1.2	25430	34	CELM08F11	U70855 Caenorhabdi
88	17	1.2	528	4	MPBS16SR	X99173 Petrocephal	c 161	17	1.2	28762	34	CEZC376	Z77336 Caenorhabdi
89	17	1.2	548	4	PBS33333	U33533 Petrocephal	162	17	1.2	30000	16	BHV130KB	Z48053 Bovine herp
90	17	1.2	804	16	ROTIDIR9	D00911 IDIR agent	c 163	17	1.2	30352	1	MTCY409	Z97188 Mycobacteri
91	17	1.2	898	7	HEVERIPS	M88255 Hevea bras	c 164	17	1.2	31896	45	CEF16D3	AC017879 Drosophil
92	17	1.2	1005	3	DOGBGALL	L23429 Canis beta-	c 165	17	1.2	32591	34	CEP16D3	Z78062 Caenorhabdi
93	17	1.2	1012	9	HS19PT009	Z96436 H.sapiens t	166	17	1.2	33359	2	U01159	U01159 Escherichia
94	17	1.2	1029	7	CALIPASB	Z30845 C.antartctic	c 167	17	1.2	33384	41	AC008915	AC008915 Homo sapi
95	17	1.2	1080	1	FPLTRAU	M34695 F.plasmiid (c 168	17	1.2	34584	34	CET27C5	Z82058 Caenorhabdi
96	17	1.2	1195	1	BUTHYBL	Z50165 B.lichenifo	c 169	17	1.2	34872	41	AC010408	AC010408 Homo sapi
97	17	1.2	1220	8	AF079296	AF079296 Melica cu	c 170	17	1.2	34877	43	AC013124	AC013124 Drosophil
98	17	1.2	1510	12	AB00515S42	AB005191 Mus muscu	c 171	17	1.2	35637	7	SPCC74	AL031543 S.pombe c
99	17	1.2	1597	40	AF020760	AF020760 Homo sapi	c 172	17	1.2	37881	34	CELM09H9	AF043700 Caenorhab
100	17	1.2	1620	4	GVITRO	Y11030 G.gallus mr	c 173	17	1.2	40739	6	AF115103	AF115103 Streptoco
101	17	1.2	1621	12	AF175324	AF175324 Mus muscu	174	17	1.2	41052	11	AC002499	AC002499 Human Cos
102	17	1.2	1705	3	BOVUROPLAK	L19542 Bovine urop	c 175	17	1.2	41055	1	SC664	AL031317 Streptomy
103	17	1.2	1769	10	HSM801100	AL117412 Homo sapi	c 176	17	1.2	41084	10	AC002500	AC002500 Human Cos
104	17	1.2	1864	9	HUMELF4AII	D30655 Homo sapien	c 177	17	1.2	41321	1	MSGY409	AD000017 Mycobacte
105	17	1.2	1872	16	BIMSPPC	L43129 Bovine immu	c 178	17	1.2	41552	34	CEC17D12	Z81473 Caenorhabdi
106	17	1.2	1881	10	S79942	S79942 ERF4A2-prot	c 179	17	1.2	41716	43	AC014073	AC014073 Drosophil
107	17	1.2	1925	7	CSZ98952	Z98952 Calymperes	c 180	17	1.2	42800	41	AC010288	AC010288 Homo sapi
108	17	1.2	1933	7	DSZ98956	Z98956 Dicranum sc	c 181	17	1.2	43802	34	CEK07F5	Z70284 Caenorhabdi
109	17	1.2	1938	4	GGU72394	U72394 Gallus gall	c 182	17	1.2	44993	43	AC014424	AC014424 Drosophil
110	17	1.2	2757	8	AF042275	AF042275 Oryza sat	c 183	17	1.2	49377	35	I88042	I88042 Sequence 1
111	17	1.2	2758	7	SCYKRO24C	Z28249 S.cerevisia	c 184	17	1.2	50714	3	AC005471	AC005471 Drosophil
112	17	1.2	2882	9	HSWUC181	X68264 H.sapiens M	c 185	17	1.2	52298	42	AC012403	AC012403 Homo sapi
113	17	1.2	3263	35	AF010326	AF010326 Drosophil	c 186	17	1.2	52359	41	AC010772	AC010772 Homo sapi
114	17	1.2	3276	12	RNTFNF1A	X84210 R.norvegicu	c 187	17	1.2	53517	32	AC002405	AC002405 Homo sapi
115	17	1.2	3283	35	AF010328	AF010328 Drosophil	c 188	17	1.2	60633	43	AC015690	AC015690 Homo sapi
116	17	1.2	3286	35	AF010327	AF010327 Drosophil	c 189	17	1.2	66489	44	AC016267	AC016267 Homo sapi
117	17	1.2	3291	35	AF010325	AF010325 Drosophil	c 190	17	1.2	67747	42	AC012630	AC012630 Homo sapi
118	17	1.2	3368	12	RNTFNF1	X84209 R.norvegicu	c 191	17	1.2	70932	10	AP000269	AP000269 Homo sapi
119	17	1.2	3450	1	XCAJ2070	AJ002070 Xanthomon	c 192	17	1.2	77118	43	AC015954	AC015954 Homo sapi
120	17	1.2	3691	7	D87895	D87895 Aspergillus	c 193	17	1.2	77201	45	AC007307	AC007307 Mus muscu
121	17	1.2	3864	40	AF096300	AF096300 Homo sapi	c 194	17	1.2	78583	41	AC009709	AC009709 Homo sapi
122	17	1.2	3970	35	AF1144386	AF114486 Drosophil	c 195	17	1.2	80470	44	AC015678	AC015678 Homo sapi
123	17	1.2	4064	9	HSU09607	U09607 Human JAK f	c 196	17	1.2	82011	41	AC009667	AC009667 Homo sapi
124	17	1.2	4266	2	AB014587	AB014587 Homo sapi	c 197	17	1.2	82692	20	AC003924	AB013476 Arabidops
125	17	1.2	4794	2	AF055586	AF055586 Vibrio ch	c 198	17	1.2	82952	7	AB015476	AB015476 Arabidops
126	17	1.2	4864	9	HSCMRP	X96395 H.sapiens m	c 199	17	1.2	83083	44	AC013671	AC013671 Homo sapi
127	17	1.2	4968	16	SH1SEQ	M81222 Herpesvirus	c 200	17	1.2	85372	8	AC005508	AC005508 Arabidops
128	17	1.2	5341	11	HSSMAD2S1	U78726 Homo sapien	c 201	17	1.2	85420	40	AC004672	AC004672 Homo sapi
129	17	1.2	5896	1	PDOXABCD	X78196 P.genitriifi	c 202	17	1.2	85943	41	AC009472	AC009472 Homo sapi

203	17	1.2	86212	7	AB010074	AB010074 Arabidops	c 276	17	1.2	177316	41	AC009456	AC009456 Homo sapi
c 204	17	1.2	87960	45	AC017906	AC017906 Drosophill	277	17	1.2	179482	32	HSDJ9264	AL132875 Homo sapi
c 205	17	1.2	88401	8	F23M19	AC007454 Arabidops	278	17	1.2	181564	44	AC010977	AC010977 Homo sapi
c 206	17	1.2	89035	8	F1511	AC006577 Sequence	c 279	17	1.2	183687	41	AC010739	AF079317 Springomo
c 207	17	1.2	89765	35	AC017970	AC017970 Drosophill	c 280	17	1.2	184457	2	AF079317	AF079317 Springomo
c 208	17	1.2	91019	35	AC001658	AC001658 Drosophill	c 281	17	1.2	185792	44	AC011028	AC011028 Homo sapi
c 209	17	1.2	91421	33	AC008105	AC008105 Homo sapi	c 282	17	1.2	186494	33	AL133323	AL133323 Homo sapi
c 210	17	1.2	93216	11	AC003016	AC003016 Human BAC	c 283	17	1.2	186557	42	AC011191	AC011191 Homo sapi
c 211	17	1.2	94281	1	AP000342	AP000342 Plasmid R	c 284	17	1.2	187886	42	AC011851	AC011851 Homo sapi
c 212	17	1.2	96964	33	AC004906	AC004906 Homo sapi	c 285	17	1.2	190014	7	AP000836	AP000836 Oriza sat
c 213	17	1.2	97487	41	AC011433	AC011433 Homo sapi	c 286	17	1.2	190528	42	AC010729	AC010729 Homo sapi
c 214	17	1.2	97542	43	AF202964	AF202964 Homo sapi	c 287	17	1.2	191356	40	AC005041	AC005041 Homo sapi
c 215	17	1.2	97854	45	AC017411	AC017411 Drosophill	c 288	17	1.2	192823	43	AC0012149	AC0012149 Homo sapi
c 216	17	1.2	98524	10	AF188025	AF188025 Homo sapi	c 289	17	1.2	193708	40	AC005035	AC005035 Homo sapi
c 217	17	1.2	100000	10	AP000032	AP000032 Homo sapi	c 290	17	1.2	195257	33	AC008177	AC008177 Homo sapi
c 218	17	1.2	100000	10	AP000103	AP000103 Homo sapi	c 291	17	1.2	195364	11	HS431A14	AC005894 Drosophill
c 219	17	1.2	100000	10	AP000179	AP000179 Homo sapi	c 292	17	1.2	196337	35	AC005894	AC005894 Drosophill
c 220	17	1.2	100666	32	CEY20C6	Z98859 Caenorhabdi	c 293	17	1.2	198303	45	AC013285	AC013285 Homo sapi
c 221	17	1.2	105325	11	HS614C15	AL035250 Human DNA	c 294	17	1.2	202291	44	ATFCA2	Z97337 Arabidops
c 222	17	1.2	105607	43	AC013410	AC013410 Homo sapi	c 295	17	1.2	202860	8	ATFCA2	Z97343 Arabidops
c 223	17	1.2	108926	40	AF042089	AF042089 Homo sapi	c 296	17	1.2	207674	8	ATFCA8	AC006719 Caenorhab
c 224	17	1.2	109016	8	ATT10K17	AL132977 Arabidops	c 297	17	1.2	207674	8	ATFCA8	AC006719 Caenorhab
c 225	17	1.2	110000	32	CEY47H9_1	Continuation (2 of	c 298	17	1.2	209365	33	AC006719	AC006719 Caenorhab
c 226	17	1.2	111390	8	AC000348	AC000348 Genomic s	c 299	17	1.2	212870	44	AC010203	AL010203 Homo sapi
c 227	17	1.2	116215	11	HS439F8	AC004130 Homo sapi	c 300	17	1.2	213721	10	HS172B20	AL022319 Human DNA
c 228	17	1.2	116490	32	HS439F8	AC004130 Homo sapi	c 301	17	1.2	213721	10	HS172B20	AL022319 Human DNA
c 229	17	1.2	120206	11	HS439F8	AL121966 Homo sapi	c 302	17	1.2	213732	2	AE001862	AE001862 Deinococc
c 230	17	1.2	121121	41	AC010580	AC010580 Drosophill	c 303	17	1.2	213732	2	AE001862	AE001862 Deinococc
c 231	17	1.2	121474	41	AC007150	AC007150 Drosophill	c 304	17	1.2	214795	42	AC012613	299116 Bacillus su
c 232	17	1.2	123872	33	AC008209	AC008209 Drosophill	c 305	17	1.2	214795	42	AC012613	299116 Bacillus su
c 233	17	1.2	125032	33	AC007099	AC007099 Homo sapi	c 306	17	1.2	217495	42	AC012613	299116 Bacillus su
c 234	17	1.2	125237	33	AC008186	AC008186 Drosophill	c 307	17	1.2	217495	42	AC012613	299116 Bacillus su
c 235	17	1.2	126813	41	AF165423	AF165423 Homo sapi	c 308	17	1.2	217495	42	AC012613	299116 Bacillus su
c 236	17	1.2	127596	42	AF165177	AF165177 Homo sapi	c 309	17	1.2	217495	42	AC012613	299116 Bacillus su
c 237	17	1.2	128230	11	HS313L4	Z99944 Human DNA s	c 310	17	1.2	217495	42	AC012613	299116 Bacillus su
c 238	17	1.2	134365	41	AC006519	AC006519 Homo sapi	c 311	17	1.2	217495	42	AC012613	299116 Bacillus su
c 239	17	1.2	135301	16	BHVLGGEN	AJ004801 Bovine he	c 312	17	1.2	217495	42	AC012613	299116 Bacillus su
c 240	17	1.2	136386	42	AC011138	AC011138 Homo sapi	c 313	17	1.2	217495	42	AC012613	299116 Bacillus su
c 241	17	1.2	138445	33	AC002979	AC002979 Homo sapi	c 314	17	1.2	217495	42	AC012613	299116 Bacillus su
c 242	17	1.2	139238	35	AC006302	AC006302 Drosophill	c 315	17	1.2	217495	42	AC012613	299116 Bacillus su
c 243	17	1.2	141258	43	AC015869	AC015869 Homo sapi	c 316	17	1.2	217495	42	AC012613	299116 Bacillus su
c 244	17	1.2	142599	11	HS413H6	AL022274 Human DNA	c 317	17	1.2	217495	42	AC012613	299116 Bacillus su
c 245	17	1.2	143174	1	D90910	D90910 Synchocyst	c 318	17	1.2	217495	42	AC012613	299116 Bacillus su
c 246	17	1.2	148126	42	AC012284	AC012284 Homo sapi	c 319	17	1.2	217495	42	AC012613	299116 Bacillus su
c 247	17	1.2	148432	35	AC004642	AC004642 Drosophill	c 320	17	1.2	217495	42	AC012613	299116 Bacillus su
c 248	17	1.2	149572	11	AC004695	AC004695 Homo sapi	c 321	17	1.2	217495	42	AC012613	299116 Bacillus su
c 249	17	1.2	149645	41	AC011510	AC011510 Homo sapi	c 322	17	1.2	217495	42	AC012613	299116 Bacillus su
c 250	17	1.2	150290	11	HS509L4	Z99496 Human DNA s	c 323	17	1.2	217495	42	AC012613	299116 Bacillus su
c 251	17	1.2	150915	32	HSDJ368B9	AL121796 Homo sapi	c 324	17	1.2	217495	42	AC012613	299116 Bacillus su
c 252	17	1.2	153561	12	MM573K1	AL076653 Homo sapi	c 325	17	1.2	217495	42	AC012613	299116 Bacillus su
c 253	17	1.2	154614	12	MM573K1	AL076653 Homo sapi	c 326	17	1.2	217495	42	AC012613	299116 Bacillus su
c 254	17	1.2	155176	11	HS453P22	AL076653 Homo sapi	c 327	17	1.2	217495	42	AC012613	299116 Bacillus su
c 255	17	1.2	155811	33	AC007413	AC007413 Drosophill	c 328	17	1.2	217495	42	AC012613	299116 Bacillus su
c 256	17	1.2	156362	35	AC008472	AC008472 Drosophill	c 329	17	1.2	217495	42	AC012613	299116 Bacillus su
c 257	17	1.2	158173	43	AC013270	AC013270 Homo sapi	c 330	17	1.2	217495	42	AC012613	299116 Bacillus su
c 258	17	1.2	158219	40	AC005534	AC005534 Homo sapi	c 331	17	1.2	217495	42	AC012613	299116 Bacillus su
c 259	17	1.2	158423	42	AC011606	AC011606 Homo sapi	c 332	17	1.2	217495	42	AC012613	299116 Bacillus su
c 260	17	1.2	159580	41	AC011432	AC011432 Homo sapi	c 333	17	1.2	217495	42	AC012613	299116 Bacillus su
c 261	17	1.2	160300	45	AC007911	AC007911 Homo sapi	c 334	17	1.2	217495	42	AC012613	299116 Bacillus su
c 262	17	1.2	160735	44	AC015821	AC015821 Homo sapi	c 335	17	1.2	217495	42	AC012613	299116 Bacillus su
c 263	17	1.2	163869	43	AC013276	AC013276 Homo sapi	c 336	17	1.2	217495	42	AC012613	299116 Bacillus su
c 264	17	1.2	164655	40	HS1108H3	AL076653 Homo sapi	c 337	17	1.2	217495	42	AC012613	299116 Bacillus su
c 265	17	1.2	164901	10	HS1108H3	AL076653 Homo sapi	c 338	17	1.2	217495	42	AC012613	299116 Bacillus su
c 266	17	1.2	165600	44	AC013394	AC013394 Homo sapi	c 339	17	1.2	217495	42	AC012613	299116 Bacillus su
c 267	17	1.2	166888	33	AC007608	AC007608 Homo sapi	c 340	17	1.2	217495	42	AC012613	299116 Bacillus su
c 268	17	1.2	167826	33	AC007404	AC007404 Homo sapi	c 341	17	1.2	217495	42	AC012613	299116 Bacillus su
c 269	17	1.2	171788	43	AC011170	AC011170 Homo sapi	c 342	17	1.2	217495	42	AC012613	299116 Bacillus su
c 270	17	1.2	171952	12	AC002324	AC002324 Mus muscu	c 343	17	1.2	217495	42	AC012613	299116 Bacillus su
c 271	17	1.2	172461	33	AC006247	AC006247 Drosophill	c 344	17	1.2	217495	42	AC012613	299116 Bacillus su
c 272	17	1.2	173810	32	HS1030M6	AL035089 Homo sapi	c 345	17	1.2	217495	42	AC012613	299116 Bacillus su
c 273	17	1.2	174050	44	AC005805	AC005805 Homo sapi	c 346	17	1.2	217495	42	AC012613	299116 Bacillus su
c 274	17	1.2	174758	33	AC005805	AC005805 Homo sapi	c 347	17	1.2	217495	42	AC012613	299116 Bacillus su
c 275	17	1.2	174758	33	AC005805	AC005805 Homo sapi	c 348	17	1.2	217495	42	AC012613	299116 Bacillus su

349	16	1.1	918	24	El1731	El1731 cDNA encodi	16	1.1	1930	7	CP298955	289855 Ceratodon p
c 350	16	1.1	951	1	PFU19743	U19743 Pseudomonas	c 423	1.1	1933	7	SAZ98958	289858 Schistidium
c 351	16	1.1	951	1	PSEOPRFH	L121202 Pseudomonas	c 424	1.1	1958	1	PSESEQB	L07613 Pseudomonas
c 352	16	1.1	962	2	AF117965	AF117965 Pseudomon	c 425	1.1	1968	7	Ptz98957	289857 Pottia trun
c 353	16	1.1	973	16	AF102782	AF102782 Banana bu	c 426	1.1	1983	35	AF181634	AF181634 Drosophill
c 354	16	1.1	981	2	AF117969	AF117969 Pseudomon	c 427	1.1	2004	1	STAQACD	M37888 Staphylococ
355	16	1.1	1000	7	LETFR5	X95903 L.esculentu	c 428	1.1	2026	4	GGU47276	U47276 Gallus gall
356	16	1.1	1004	3	BTCNF1	Z48477 B.taurus mR	c 429	1.1	2038	1	ECXERB	X15130 E. coli xer
c 357	16	1.1	1018	12	RATCPS113	M12335 Rat nucleus	c 430	1.1	2061	5	E08061	E08061 DNA encodin
c 358	16	1.1	1041	2	AF044794	AF044794 Neisseria	c 431	1.1	2061	5	I23834	I23834 Sequence 9
c 359	16	1.1	1047	2	AF090797	AF090797 Neisseria	c 432	1.1	2061	5	I43345	I43345 Sequence 5
c 360	16	1.1	1054	2	BCr15704	Y15704 Bacillus ci	c 433	1.1	2061	5	I44694	I44694 Sequence 5
c 361	16	1.1	1065	10	AF007782	AF007782 Homo sapi	c 434	1.1	2076	35	AF188888	AF188888 Musca dom
c 362	16	1.1	1071	1	NGU75635	U75635 Neisseria g	c 435	1.1	2090	1	PAU17232	U17232 Pseudomonas
c 363	16	1.1	1071	1	NGU75636	U75636 Neisseria g	c 436	1.1	2107	34	DDIADCYA03	L05498 Dictyostelli
c 364	16	1.1	1075	8	SST242803	AJ242803 Sporobolu	c 437	1.1	2108	9	D50914	D50914 Human mRNa
c 365	16	1.1	1103	12	D78265	D78265 Mus musculu	c 438	1.1	2130	11	AF078107	AF078107 Homo sapi
c 366	16	1.1	1105	9	HSXN2GEN	X89851 H.sapiens d	c 439	1.1	2157	5	AR054117	AR054117 Sequence
c 367	16	1.1	1122	1	STLEUB	X53376 S.typhimuri	c 440	1.1	2157	9	HSRMRNA	X59155 H.sapiens r
c 368	16	1.1	1125	16	PAYCP	D50591 Papaya ring	c 441	1.1	2161	9	HSRECLL	X57303 H.sapiens R
c 369	16	1.1	1126	12	RNCFPSIX38	D27513 R.norvegicu	c 442	1.1	2169	12	NMU132236	AJ132236 Mus muscu
c 370	16	1.1	1148	5	E12704	E12704 Papaya ring	c 443	1.1	2195	1	ECOEYBBD	M28819 E.coli exbb
c 371	16	1.1	1151	7	PCUL1717	U17117 Pneumocysti	c 444	1.1	2224	34	DME243607	AJ243607 Drosophill
c 372	16	1.1	1152	34	AB010284	AB010284 Trypanoso	c 445	1.1	2232	1	DEPEPCAR	X86443 E.coli pepa
c 373	16	1.1	1279	4	AB022691	AB022691 Xenopus 1	c 446	1.1	2415	1	D87842	D87842 Escherichia
c 374	16	1.1	1287	12	MUSCYPC	M74227 Mouse cyclo	c 447	1.1	2415	1	STGYRB	Y07916 S.typhimuri
c 375	16	1.1	1288	4	XLEIF4AI	Y12590 X.laevis mR	c 448	1.1	2415	1	STGYRBOR	Y08383 S.typhimuri
c 376	16	1.1	1288	5	I14303	I14303 Sequence 4	c 449	1.1	2472	2	NMU79481	U79481 Neisseria m
c 377	16	1.1	1300	1	STU20795	U20795 Salmonella	c 450	1.1	2502	1	BACCDG	M12777 B.meceras
c 378	16	1.1	1320	2	RMW53475	U51475 Rhizobium m	c 451	1.1	2508	12	RNUDPNAGE	Y07744 R.norvegicu
c 379	16	1.1	1348	1	ESU13036	U13036 Eubacterium	c 452	1.1	2512	12	D78264	D78264 Mus musculu
c 380	16	1.1	1351	16	AF120270	AF120270 Papaya r1	c 453	1.1	2552	34	DME243599	AJ243599 Drosophill
c 381	16	1.1	1357	35	MSU11879	U11879 Manduca sex	c 454	1.1	2631	1	BCCEQT	X59045 B.macerans
c 382	16	1.1	1364	34	MOTP4	M64346 Manduca sex	c 455	1.1	2670	1	CXCEQI	Z34099 C.equi DNA
c 383	16	1.1	1375	1	PP16SRRL19	D14154 Peptostrept	c 456	1.1	2683	1	BAJ10128	AJ010128 Bacillus
c 384	16	1.1	1401	1	ESR1BRNAL	Z36271 Eubacterium	c 462	1.1	2692	16	PRVNIIBCTP	X96538 Papaya ring
c 385	16	1.1	1401	35	CPU43545	U43545 Culex pipie	c 457	1.1	2752	34	CBU45326	U45326 Caenorhabdi
c 386	16	1.1	1421	34	MSLMTFRGA	M83761 Mytilus edu	c 459	1.1	2781	34	SRN1337	S1337 18S rRNA [A
c 387	16	1.1	1436	6	P29P3P4	J02479 Bacterioph	c 460	1.1	2791	9	H81NARS6K	X85106 H.sapiens m
c 388	16	1.1	1440	4	SSAJ664	AJ000664 Salmo sal	c 461	1.1	2798	1	XGPRONEA	X51635 X.campestri
c 389	16	1.1	1475	2	SEU43309	U43309 Salmonella	c 462	1.1	2808	7	ECOPRKA	L27821 Oryza sativ
c 390	16	1.1	1476	1	SEU433313	U33313 Pseudomonas	c 463	1.1	2812	1	ECOSNGLPD	M55989 E.coli sn-g
c 391	16	1.1	1479	1	DNEP53PS	Z29339 D.nodosus (c 464	1.1	2831	1	SSQACFPREP	Z37964 Staphylococ
c 392	16	1.1	1479	5	AR038196	AR038196 Sequence	c 465	1.1	2838	1	EGOGLPDA	D00425 E. coli glp
c 393	16	1.1	1479	5	I44026	I44026 Sequence 68	c 466	1.1	2847	12	CGPRU28A	X79298 C.griseus r
c 394	16	1.1	1479	5	I49035	I49035 Sequence 68	c 467	1.1	2936	1	ECBPBA	X04515 E. coli bpb
c 395	16	1.1	1480	4	SSAJ665	AJ000665 Salmo sal	c 468	1.1	2940	8	AF180367	AF180367 Aspergill
c 396	16	1.1	1533	35	AF132170	AF132170 Drosophill	c 469	1.1	2960	16	PRVNIAB	X78557 Papaya ring
c 397	16	1.1	1534	34	TCSSTUB	L23506 Trichostro	c 470	1.1	2962	8	CRU73856	X73856 Chlamydomon
c 398	16	1.1	1542	7	CROE3	X13832 C.reinhardt	c 471	1.1	3025	2	AF047363	AF047363 Paenibaci
c 399	16	1.1	1561	16	U87663	H7663 Hepatitis G	c 472	1.1	3092	8	ZNA17898	Y17898 Zea mays mR
c 400	16	1.1	1600	4	XLEIF4AII	Y12591 X.laevis mR	c 473	1.1	3099	1	BACBGLH	D17519 Bacillus ci
c 401	16	1.1	1601	35	AF092910	AF092910 Trypanoso	c 474	1.1	3100	2	S67033	S67033 beta-1,3-g1
c 402	16	1.1	1620	40	HUM56KINB	L07598 Homo sapien	c 475	1.1	3111	1	PSECUMEL	D63377 Pseudomonas
c 403	16	1.1	1656	7	BLYRCAB	M55448 Hordeum vul	c 476	1.1	3204	40	AF127035	AF127035 Homo sapi
c 404	16	1.1	1662	12	CPO238589	AJ238589 Cavia por	c 477	1.1	3219	7	SCDCD39	X04289 Yeast cell
c 405	16	1.1	1674	34	DROSILTBGF	M23543 Drosophila	c 478	1.1	3234	1	PSEPAIG	D28587 Pseudomonas
c 406	16	1.1	1679	4	AF001299	AF001299 Danio rer	c 479	1.1	3240	1	SAAJ5198	AJ005198 Streptomy
c 407	16	1.1	1694	34	BMJ000916	AD000916 Brugia ma	c 480	1.1	3240	1	SAAJ5198	AJ005198 Streptomy
c 408	16	1.1	1695	1	MSGY414B	AD000011 Mycobacte	c 481	1.1	3240	1	SAN6517	AJ006517 Streptomy
c 409	16	1.1	1720	12	RNU52276	U55276 Rattus norv	c 482	1.1	3240	1	SAN6517	AJ006517 Streptomy
c 410	16	1.1	1722	16	LCV16308	Y16308 Lymphocyti	c 483	1.1	3288	10	HSU41387	U41387 Human Gu pr
c 411	16	1.1	1728	9	HUMHPSA	D61391 Human mRNA	c 484	1.1	3617	12	RATLLIPA	L03294 Rattus norv
c 412	16	1.1	1738	3	AF076281	AF076281 Mustela v	c 485	1.1	3648	34	AB008449	AB008449 Bombyx mo
c 413	16	1.1	1758	1	PAAMPC	X34719 P. aerugin	c 486	1.1	3680	8	AF093639	AF093639 Linum usi
c 414	16	1.1	1760	16	AF063220	AF063220 Papaya r1	c 487	1.1	3693	9	HUMPPROA	M63635 Human glyci
c 415	16	1.1	1763	16	AF063221	AF063221 Papaya r1	c 488	1.1	3720	1	AERPONG	X66793 A.eutrophus
c 416	16	1.1	1791	34	AB013012	AB013012 Doliolum	c 489	1.1	3750	35	AF033823	AF033823 Drosophill
c 417	16	1.1	1811	1	STPEPMG	X55778 S.typhimur	c 490	1.1	3755	35	AC008239	AC008239 Leishmani
c 418	16	1.1	1840	2	XANPELY	L38573 S.typhimur	c 491	1.1	3762	9	HUMPP	M64590 Human glyci
c 419	16	1.1	1845	35	AF099185	AF099185 Drosophill	c 492	1.1	3776	1	CFIB14C	L38827 Cellulomona
c 420	16	1.1	1857	1	D89826	D89826 Escherichia	c 493	1.1	3783	9	HUNGDCMR	D90239 Human mRNa
c 421	16	1.1	1871	12	NMU36274	U36274 Mus musculu	c 494	1.1	3822	7	BLVAC1L	M57533 Hordeum vul

495	16	1.1	3891	35	AF071502	AF071502 Drosophil	568	16	1.1	10437	2	AE000245	AE000245 Escherich
496	16	1.1	3927	34	AF043629	AF043629 Toxoplas	c 569	16	1.1	10492	35	DMU34925	U34925 Drosophila
c 497	16	1.1	4124	7	BOISR	X56978 B.oleracea	c 570	16	1.1	10617	1	BSY14077	Y14077 Bacillus su
c 498	16	1.1	4211	9	HSDRES9	X98654 H.sapiens m	c 571	16	1.1	10731	2	AE000163	AE000163 Escherich
c 499	16	1.1	4307	9	HSTYL	X99688 H.sapiens m	c 572	16	1.1	10776	2	AE000418	AE000418 Escherich
c 500	16	1.1	4329	7	AWTAM4	X59057 A.majus tra	c 573	16	1.1	11053	2	AE000286	AE000286 Escherich
c 501	16	1.1	4348	7	BORR2518	X60324 B.oleracea	c 574	16	1.1	11166	2	AE000203	AE000203 Deinococc
c 502	16	1.1	4354	35	MSU09650	U09650 Manduca sex	c 575	16	1.1	11317	2	AE000945	AE000945 Archaeogl
c 503	16	1.1	4417	1	AB019513	AB019513 Streptomy	c 576	16	1.1	11355	2	AE000447	AE000447 Escherich
c 504	16	1.1	4474	5	I58526	I58526 Sequence 9	c 577	16	1.1	11566	2	U32732	U32732 Haemophilus
c 505	16	1.1	4474	5	I87001	I87001 Sequence 9	c 578	16	1.1	11680	2	AE001258	AE001258 Treponema
c 506	16	1.1	4509	40	AF168791	AF168791 Homo sapi	c 579	16	1.1	11694	2	AE000383	AE000383 Escherich
c 507	16	1.1	4515	35	AF0126540	AF0126540 Drosophil	c 580	16	1.1	11910	9	HUMHRX	L04284 Human germ
c 508	16	1.1	4535	40	AF078622	AF078622 Homo sapi	c 581	16	1.1	11929	2	AE000496	AE000496 Escherich
c 509	16	1.1	4607	8	AF093648	AF093648 Linum usi	c 582	16	1.1	11931	12	CGRHOD	X61084 C.griseus r
c 510	16	1.1	4622	8	AF093641	AF093641 Linum usi	c 583	16	1.1	12276	43	AC013930	AC013930 Drosophil
c 511	16	1.1	4627	8	AF093638	AF093638 Linum usi	c 584	16	1.1	12323	2	BSP250862	AJ250862 Bacillus
c 512	16	1.1	4631	11	HGU72391	U72391 Human neoge	c 585	16	1.1	12551	2	AE000598	AE000598 Helicobac
c 513	16	1.1	4637	8	AF093640	AF093640 Linum usi	c 586	16	1.1	12663	2	AE000168	AE000168 Escherich
c 514	16	1.1	4637	8	AF093643	AF093643 Linum usi	c 587	16	1.1	12965	2	AE0002048	AE0002048 Deinococc
c 515	16	1.1	4637	8	AF093644	AF093644 Linum usi	c 588	16	1.1	13163	2	AE001042	AE001042 Archaeogl
c 516	16	1.1	4651	8	AF093645	AF093645 Linum usi	c 589	16	1.1	13638	11	AC005573	AC005573 Homo sapi
c 517	16	1.1	4780	7	ATHTOP2	L21015 Arabidopsis	c 590	16	1.1	13831	2	AE000707	AE000707 Aquifex a
c 518	16	1.1	4809	11	AF038385	AF038385 Homo sapi	c 591	16	1.1	14097	2	AE001093	AE001093 Archaeogl
c 519	16	1.1	4841	7	LUU27081	U27081 Linum usita	c 592	16	1.1	14255	5	I43726	I43726 Sequence 1
c 520	16	1.1	4931	1	ECGYRBF	X04341 E. coli gen	c 593	16	1.1	14255	5	I43760	I43760 Sequence 1
c 521	16	1.1	4970	40	AF107403	AF107403 Homo sapi	c 594	16	1.1	14255	5	I96218	I96218 Sequence 55
c 522	16	1.1	4991	1	BLO242596	AJ242596 Bifidobac	c 595	16	1.1	14255	5	HUMTRLALL1	L04731 Homo sapien
c 523	16	1.1	5029	1	PSETBMAF	L40033 Pseudomonas	c 596	16	1.1	14529	34	CET25G3	Z72516 Caenorhabdi
c 524	16	1.1	5197	8	LES6379	AO06379 Lycopersi	c 597	16	1.1	14529	34	D90834	D90834 E.coli geno
c 525	16	1.1	5230	1	TPU28219	U28219 Treponema p	c 598	16	1.1	14930	43	AC013987	AC013987 Drosophil
c 526	16	1.1	5240	12	MMU131021	AJ131021 Mus muscu	c 599	16	1.1	15180	43	AC013987	D90833 E.coli geno
c 527	16	1.1	5263	1	RLRES	X98117 Rhizobium l	c 600	16	1.1	15640	2	AE000968	AE000968 Archaeogl
c 528	16	1.1	5297	10	HSU61262	U61262 Human neoge	c 601	16	1.1	15705	1	D90788	D90788 E.coli geno
c 529	16	1.1	5305	7	CHSOFSA	X04131 Spinach pla	c 602	16	1.1	15807	1	MEU72662	U72662 Methylobact
c 530	16	1.1	5390	43	AC009515	AC009515 Staphyloc	c 603	16	1.1	15855	41	AC010290	AC010290 Homo sapi
c 531	16	1.1	5401	34	DMSLIT	X53959 Drosophila	c 604	16	1.1	16637	41	AC010371	AC010371 Homo sapi
c 532	16	1.1	5479	8	AF093642	AF093642 Linum usi	c 605	16	1.1	16929	43	AC012987	AC012987 Drosophil
c 533	16	1.1	5482	2	BCU19883	U19883 Burkholderi	c 606	16	1.1	17871	12	AF110420	AF110420 Mus muscu
c 534	16	1.1	5521	2	AF105219	AF105219 Thermomon	c 607	16	1.1	18271	12	SCF76	AL121600 Streptomy
c 535	16	1.1	5541	5	AR012071	AR012071 Sequence	c 610	16	1.1	18292	2	D90704	D90704 Escherichia
c 536	16	1.1	5541	5	AR025196	AR025196 Sequence	c 611	16	1.1	18571	1	D90789	D90789 E.coli geno
c 537	16	1.1	5541	5	AR038653	AR038653 Sequence	c 612	16	1.1	18918	1	D90700	D90700 Escherichia
c 538	16	1.1	5541	5	AR068500	AR068500 Sequence	c 613	16	1.1	18994	1	D90700	AE001708 Thermotog
c 539	16	1.1	5594	1	PPY09450	Y09450 P.putida pl	c 614	16	1.1	19531	41	AC010229	AC010229 Homo sapi
c 540	16	1.1	5708	6	POP29B	V01155 Left end of	c 615	16	1.1	19588	41	AC016569	AC016569 Homo sapi
c 541	16	1.1	5715	9	AB023157	AB023157 Homo sapi	c 616	16	1.1	20042	44	AC016569	AE001209 Treponema
c 542	16	1.1	5751	9	HUMMLL	D14540 Human mRNA	c 617	16	1.1	20278	2	AE001209	U56960 Caenorhabdi
c 543	16	1.1	5924	8	AF093646	AF093646 Linum usi	c 618	16	1.1	20787	34	CELF25H10	Z68341 Caenorhabdi
c 544	16	1.1	6111	10	AB033029	AB033029 Homo sapi	c 619	16	1.1	20891	34	CEF01G4	AC008593 Homo sapi
c 545	16	1.1	6125	1	PSEPSTD	D45195 Pseudomonas	c 620	16	1.1	21038	41	AC008593	Z75535 Caenorhabdi
c 546	16	1.1	6166	8	AF093649	AF093649 Linum usi	c 621	16	1.1	21189	34	CEF14B4	AC010381 Homo sapi
c 547	16	1.1	6296	9	D87432	D87432 Human mRNA	c 622	16	1.1	21589	41	AC010381	L32093 Pedicoccus
c 548	16	1.1	6310	4	ACSWOPS3	AF134194 Anolis ca	c 623	16	1.1	21838	1	PDCAFOBER	Z32771 P.pentoscac
c 549	16	1.1	6393	1	HU19730	U19730 Haemophilus	c 624	16	1.1	21839	1	PEPSTROP	AL080237 Arabidops
c 550	16	1.1	6536	12	MUSALCR01	L36825 Mus Musculu	c 625	16	1.1	22145	8	ATF313	D83967 Bacillus su
c 551	16	1.1	6693	35	AF070064	AF070064 Drosophil	c 626	16	1.1	22916	34	CEF53H10	Z77664 Caenorhabdi
c 552	16	1.1	6751	34	CELMYOD	M59940 Caenorhabdi	c 627	16	1.1	23332	7	AC014464	AC014464 Drosophil
c 553	16	1.1	6940	11	HUMMLAF4F	L22179 Human MLL-A	c 628	16	1.1	23476	43	AC014464	AB025641 Arabidops
c 554	16	1.1	7222	12	MUSMA	D29801 Mouse mRNA	c 629	16	1.1	23830	8	SPAC27F1	Z69368 S.pombe chr
c 555	16	1.1	7290	1	BACCCOS	D70843 Bacillus st	c 630	16	1.1	23906	2	AF176314	AF176314 Zymomonas
c 556	16	1.1	8404	9	HUMHT31	D26351 Human mRNA	c 631	16	1.1	24411	41	AC008534	AC008534 Homo sapi
c 557	16	1.1	8421	34	DVU39746	M53449 Hordeum vul	c 632	16	1.1	24555	45	AC017315	AF140550 Salmonell
c 558	16	1.1	8766	7	BLRYCABG	U01062 Human type	c 633	16	1.1	25252	2	AF140550	AB017765 Trypanoso
c 559	16	1.1	8833	11	HUMIFP3R3	D85415 Pseudomonas	c 634	16	1.1	25795	41	AC008911	AC008911 Homo sapi
c 560	16	1.1	9239	1	D85415	AR053191 Sequence	c 635	16	1.1	26007	1	BSY14083	Y14083 Bacillus su
c 561	16	1.1	9432	5	I50752	I50752 Sequence 1	c 636	16	1.1	26402	43	AC013906	AC013906 Drosophil
c 562	16	1.1	9432	5	I50752	Z97831 Mycobacteri	c 637	16	1.1	26462	43	AC012932	AC012932 Drosophil
c 563	16	1.1	9532	1	MTY20G10	AB009689 Mus muscu	c 638	16	1.1	26536	2	AE001244	AE001244 Treponema
c 564	16	1.1	9677	12	AE009689	AE009689 Helicobac	c 639	16	1.1	27060	43	AC014005	AC014005 Drosophil
c 565	16	1.1	10134	2	AE001488	X97251 Papaya ring	c 640	16	1.1	27555	43	AC012903	AC012903 Drosophil
c 566	16	1.1	10326	16	PRSVGEN	AE001236 Treponema							
567	16	1.1	10340	2	AE001236								

641	16	1.1	27602	34	CET01C1	714	16	1.1	42729	1	MTCY71	292771 Mycobacteri
642	16	1.1	28168	34	CET37H9A	c 715	16	1.1	42776	34	CEP15D4	280344 Caenorhabdi
c 643	16	1.1	29624	35	CEUB0545	716	16	1.1	42968	34	CEY37ALA	292970 Caenorhabdi
c 644	16	1.1	30034	8	OSU705A1	717	16	1.1	43075	6	U88974	U88974 Streptococ
645	16	1.1	30148	34	CEP57C7	c 718	16	1.1	43190	11	AC005777	AC005777 Homo sapi
646	16	1.1	30419	35	CELT07H8	719	16	1.1	43430	1	MTCY16B7	281331 Mycobacteri
c 647	16	1.1	30941	1	SC4C6	c 720	16	1.1	43516	10	AP000401	AP000401 Homo sapi
648	16	1.1	31312	10	AP000283	721	16	1.1	44090	33	AC006784	AC006784 Caenorhab
649	16	1.1	31638	1	RMEXPGNS	722	16	1.1	44725	40	AF036405	AF036405 Homo sapi
c 650	16	1.1	31795	34	CELT07H6	723	16	1.1	45000	43	AC013257	AC013257 Leishmani
651	16	1.1	31913	43	AC013216	c 724	16	1.1	45701	43	AC014674	AC014674 Drosophill
c 652	16	1.1	31975	8	SPCC553	c 725	16	1.1	45932	43	AC015155	AC015155 Drosophill
c 653	16	1.1	32039	1	SC7A1	c 726	16	1.1	46375	6	AF064539	AF064539 Bacterioph
654	16	1.1	32106	10	AP000284	c 727	16	1.1	46445	2	AF051917	AF051917 Staphyloc
655	16	1.1	32195	20	AC004154	c 728	16	1.1	46582	43	AC012831	AC012831 Drosophill
c 656	16	1.1	32566	34	CEY94A7B	729	16	1.1	47263	41	AC010425	AC010425 Homo sapi
c 657	16	1.1	32806	32	HSJ819L10	730	16	1.1	47815	41	AC009563	AC009563 Homo sapi
c 658	16	1.1	33550	11	AC003004	731	16	1.1	47852	1	MTV023	AL020222 Mycobacte
c 659	16	1.1	33896	35	CELT05A8	c 732	16	1.1	48295	44	AC010749	AC010749 Homo sapi
c 660	16	1.1	33930	34	CEK04H4	733	16	1.1	48574	44	AC016602	AC016602 Homo sapi
c 661	16	1.1	33954	7	SC9905	c 734	16	1.1	49027	42	AC011727	AC011727 Homo sapi
c 662	16	1.1	34083	2	AF124757	735	16	1.1	50149	44	AC016083	AC016083 Homo sapi
c 663	16	1.1	34150	1	MTCY190	736	16	1.1	50302	45	AC017148	AC017148 Drosophill
664	16	1.1	34238	32	CEV45F10_4	c 737	16	1.1	50969	43	AC014793	AC014793 Drosophill
c 665	16	1.1	34774	43	AC013899	c 738	16	1.1	50997	41	AC010679_3	Continuation (4 of
c 666	16	1.1	34860	34	CEUR173	c 739	16	1.1	52001	11	HSB691018	AL080238 Human DNA
667	16	1.1	35292	1	MTCY3C7	740	16	1.1	52094	32	T16118	AL049915 Arabidops
668	16	1.1	35424	43	AC013816	741	16	1.1	52297	6	MLCGA	218946 Mycobacteri
669	16	1.1	35559	6	PABY13918	742	16	1.1	54252	7	AB017060	AB017060 Arabidops
c 670	16	1.1	35580	6	AB008550	743	16	1.1	54488	43	AC013814	AC013814 Homo sapi
671	16	1.1	35737	11	AC005263	c 744	16	1.1	54527	43	AC015174	AC015174 Drosophill
672	16	1.1	35743	8	CELF31E8	745	16	1.1	55466	43	AC013616	AC013616 Homo sapi
673	16	1.1	35769	8	SPAC23A1	746	16	1.1	57166	40	AC009320	AC009320 Homo sapi
674	16	1.1	36330	1	MTY20B11	c 747	16	1.1	57236	42	AC009878	AC009878 Homo sapi
c 675	16	1.1	36615	43	AC014144	748	16	1.1	57352	44	AC016317	AC016317 Homo sapi
c 676	16	1.1	37186	1	MSGY244	c 749	16	1.1	57517	42	AC010563	AC010563 Drosophill
c 677	16	1.1	37218	11	HSN11D4	750	16	1.1	57634	42	AC010702	AC010702 Drosophill
c 678	16	1.1	37225	34	CEC17B4	751	16	1.1	58527	7	AB007649	AB007649 Arabidops
c 679	16	1.1	37307	10	HS335H7	752	16	1.1	58713	41	AC009494	AC009494 Homo sapi
c 680	16	1.1	37394	8	SPAC2F3	753	16	1.1	58903	44	AC016104	AC016104 Homo sapi
681	16	1.1	37439	34	CEP35E2	c 754	16	1.1	61151	44	AC016416	AC016416 Homo sapi
682	16	1.1	37462	43	AC013090	c 755	16	1.1	61845	43	AC013765	AC013765 Homo sapi
683	16	1.1	37470	35	CELH14E04	c 756	16	1.1	62198	43	AC013832	AC013832 Drosophill
c 684	16	1.1	37693	10	AP000522	c 757	16	1.1	62608	44	AC016784	AC016784 Homo sapi
c 685	16	1.1	37821	1	MLCB1770	c 758	16	1.1	62944	10	HSMHC3W2A	U89336 Human HLA c
c 686	16	1.1	38548	8	SPBC21B10	c 759	16	1.1	62953	43	AC016121	AC016121 Homo sapi
c 687	16	1.1	38563	34	CET20B3	760	16	1.1	63441	45	AC012554	AC012554 Homo sapi
688	16	1.1	38715	11	CH19R28051	761	16	1.1	63681	45	AC015996	AC015996 Homo sapi
c 689	16	1.1	39146	10	CH19R28051	762	16	1.1	63751	45	AC017489	AC017489 Drosophill
c 690	16	1.1	39480	34	CEC34C6	c 763	16	1.1	64044	8	SCE9163	U18922 Saccharomyc
691	16	1.1	39752	35	CEC04F5	c 764	16	1.1	64211	40	AC000054	AC000054 , complet
c 692	16	1.1	39839	43	AC013000	c 765	16	1.1	64797	8	SCE9747	U18839 Saccharomyc
693	16	1.1	40018	7	AP000740	766	16	1.1	64957	1	AB032367	AB032367 Streptomy
694	16	1.1	40162	40	U58675	767	16	1.1	67042	41	AC009939	AC009939 Homo sapi
695	16	1.1	40320	43	AC015387	c 768	16	1.1	67042	41	AC009939	AC009939 Homo sapi
696	16	1.1	40397	7	SC9959	c 769	16	1.1	68203	42	AC012427	AC012427 Homo sapi
697	16	1.1	40442	2	SCI8	c 770	16	1.1	68203	42	AC012427	AC012427 Homo sapi
698	16	1.1	40665	35	CELC27F2	c 771	16	1.1	68726	7	AB017063	AB017063 Arabidops
c 699	16	1.1	40665	35	CELC27F2	c 772	16	1.1	69493	43	AC014818	AC014818 Drosophill
700	16	1.1	40880	7	SPCC1235	c 773	16	1.1	69516	45	AC016851	AC016851 Homo sapi
c 701	16	1.1	40965	42	AC012633	c 774	16	1.1	69673	2	AF102990	AF102990 Versinia
702	16	1.1	41009	32	CEY94A7	775	16	1.1	70095	41	AC008980	AC008980 Homo sapi
c 703	16	1.1	41037	45	AC017476	c 776	16	1.1	70311	8	AF128457	AF128457 Oryza sat
c 704	16	1.1	41071	34	CELB0303	c 777	16	1.1	70661	44	AC016422	AC016422 Homo sapi
c 705	16	1.1	41397	34	CEB0285	c 778	16	1.1	70865	43	AC015476	AC015476 Homo sapi
706	16	1.1	41594	41	AC010964	c 779	16	1.1	71097	8	F15K9	AC005278 Arabidops
c 707	16	1.1	41625	10	HS171R	c 780	16	1.1	71214	45	AC017250	AC017250 Drosophill
c 708	16	1.1	41625	10	HS171R	c 781	16	1.1	71907	43	AC014585	AC014585 Drosophill
c 709	16	1.1	41848	33	AC006098	c 782	16	1.1	72164	32	HS409J21	283824 Homo sapien
710	16	1.1	41906	1	SC5C7	c 783	16	1.1	72401	41	AC008389	AC008389 Homo sapi
c 711	16	1.1	42282	34	CELB0304	c 784	16	1.1	72438	2	ECOUW67_3	Continuation (4 of
c 712	16	1.1	42418	32	HSN38G6	785	16	1.1	72975	44	AC016354	AC016354 Homo sapi
c 713	16	1.1	42660	34	CEP15D3	c 786	16	1.1	73087	10	HS147M19	AL021978 Homo sapi

c 787	16	1.1	73491	43	AC009641	Homo sapi	860	16	1.1	100000	10	AP000109	AP000109 Homo sapi
c 788	16	1.1	73635	50	ATAC011915	Arabidops	861	16	1.1	100000	10	AP000131	AP000131 Homo sapi
c 789	16	1.1	73739	35	AC001646	Drosophil	862	16	1.1	100000	10	AP000153	AP000153 Homo sapi
c 790	16	1.1	74780	33	AC005445	Drosophil	863	16	1.1	100000	10	AP000185	AP000185 Homo sapi
c 791	16	1.1	75079	43	AC015047	Drosophil	864	16	1.1	100000	10	AP000209	AP000209 Homo sapi
c 792	16	1.1	75263	41	AC009835	Homo sapi	865	16	1.1	100000	41	AC008366	AC008366 Drosophil
c 793	16	1.1	75263	41	AC009835	Homo sapi	c 866	16	1.1	100364	40	AC007590	AC007590 Homo sapi
c 794	16	1.1	76743	35	AC005473	Drosophil	867	16	1.1	100590	42	AC010023	AC010023 Drosophil
c 795	16	1.1	77618	45	AC017020	Homo sapi	868	16	1.1	101340	45	AC018104	AC018104 Drosophil
c 796	16	1.1	78189	44	AC015737	Homo sapi	c 869	16	1.1	102004	8	ATAC005395	ATAC005395 Arabidops
c 797	16	1.1	78205	43	AC015748	Homo sapi	870	16	1.1	102739	11	HS671014	HS671014 Human DNA
c 798	16	1.1	78505	33	AC006408	Homo sapi	871	16	1.1	103370	41	AC009352	AC009352 Drosophil
c 799	16	1.1	79109	7	AB016871	Arabidops	c 872	16	1.1	103632	8	AF074021	AF074021 Arabidops
c 800	16	1.1	79114	33	AC005475	Drosophil	c 873	16	1.1	104059	42	AC010110	AC010110 Drosophil
c 801	16	1.1	79227	10	HS148E22	Human DNA	c 874	16	1.1	104081	11	HSDJ263J7	AL049545 Human DNA
c 802	16	1.1	79528	11	HS466N1	297630 Human DNA s	875	16	1.1	104163	50	AC010155	AC010155 Genomic s
c 803	16	1.1	79706	7	AB020746	AB020746 Arabidops	c 876	16	1.1	105326	43	AC014828	AC014828 Drosophil
c 804	16	1.1	79740	42	AC009905	AC009905 Drosophil	c 877	16	1.1	105320	32	AP000668	AP000668 Homo sapi
c 805	16	1.1	80000	46	AC005652	AC005652 *** SEQUE	c 878	16	1.1	105788	32	AP000749	AP000749 Homo sapi
c 806	16	1.1	80389	35	AC005643	AC005643 Drosophil	c 879	16	1.1	105809	43	AC013758	AC013758 Homo sapi
c 807	16	1.1	80393	7	AP000382	AP000382 Arabidops	880	16	1.1	105816	45	AC017069	AC017069 Homo sapi
c 808	16	1.1	80445	35	AC004288	AC004288 Drosophil	881	16	1.1	106273	11	HSJ1018A4	AL109612 Human DNA
c 809	16	1.1	80818	42	AC009732	AC009732 Drosophil	882	16	1.1	106723	42	AC010064	AC010064 Drosophil
c 810	16	1.1	81487	11	HSJ770C23	AL118509 Human DNA	883	16	1.1	106953	33	AC006982	AC006982 Homo sapi
c 811	16	1.1	81786	11	AC003002	AC003002 Human DNA	884	16	1.1	108879	33	AC004804	AC004804 Homo sapi
c 812	16	1.1	82359	40	AC004922	AC004922 Homo sapi	885	16	1.1	108906	32	AP000796	AP000796 Homo sapi
c 813	16	1.1	82503	7	AB016886	AB016886 Arabidops	c 886	16	1.1	109566	33	AC007803	AC007803 Drosophil
c 814	16	1.1	83253	7	AP000383	AP000383 Arabidops	c 887	16	1.1	109826	33	AC008311	AC008311 Drosophil
c 815	16	1.1	83605	43	AC014199	AC014199 Drosophil	888	16	1.1	110000	32	CEY102A5_0	299711 Caenorhabdi
c 816	16	1.1	83693	8	ATT13J8	AL035524 Arabidops	c 889	16	1.1	110000	32	CEY116A8_2	Continuation (3 of
c 817	16	1.1	83922	8	T9A4	AF096373 Arabidops	890	16	1.1	110000	32	CEY37H9_1	AL022596 Caenorhab
c 818	16	1.1	84246	34	AC002512	AC002512 Drosophil	c 891	16	1.1	110000	32	CEY47H9_1	Continuation (2 of
c 819	16	1.1	84305	41	AC006943	AC006943 Mus muscu	892	16	1.1	110000	32	CEY47H9_3	Continuation (4 of
c 820	16	1.1	84323	10	HS138B7	Z98752 Human DNA s	893	16	1.1	110000	32	CEY48G10_1	Continuation (2 of
c 821	16	1.1	85561	8	ATAC009326	AC009326 Arabidops	894	16	1.1	110000	32	CEY53C10_0	293340 Caenorhabdi
c 822	16	1.1	85674	40	AF164343	AF164343 Homo sapi	895	16	1.1	110000	32	CEY53C10_1	Continuation (2 of
c 823	16	1.1	85740	43	AC014942	AC014942 Drosophil	896	16	1.1	110000	32	CEY53C10_3	Continuation (4 of
c 824	16	1.1	86643	42	AC012321	AC012321 Homo sapi	c 897	16	1.1	110000	32	CEY73F8_1	Continuation (2 of
c 825	16	1.1	86599	7	AB009050	AB009050 Arabidops	c 898	16	1.1	110000	32	CEY81G3_2	Continuation (3 of
c 826	16	1.1	87077	40	HUAC004097	AC004097 Human Chr	899	16	1.1	110000	33	AC007194_1	Continuation (2 of
c 827	16	1.1	87210	7	AB011485	AB011485 Arabidops	c 900	16	1.1	110000	41	AC008691_1	Continuation (2 of
c 828	16	1.1	88178	44	AC011787	AC011787 Homo sapi	c 901	16	1.1	110000	41	AC011455_0	AC011455 Homo sapi
c 829	16	1.1	88413	8	ATAC005724	AC005724 Arabidops	902	16	1.1	110926	41	AC009846	AC009846 Drosophil
c 830	16	1.1	88512	8	F21H2	AC007894 Arabidops	c 903	16	1.1	111723	11	HSJ101K10	AL080275 Human DNA
c 831	16	1.1	89086	10	HS1188J21	AL109563 Human DNA	904	16	1.1	111732	33	AC006015	AC006015 Homo sapi
c 832	16	1.1	89448	40	AC005067	AC005067 Homo sapi	905	16	1.1	112074	9	AP000012	AP000012 Homo sapi
c 833	16	1.1	90390	42	AC009377	AC009377 Drosophil	906	16	1.1	112710	32	HSJ136014	AL121963 Homo sapi
c 834	16	1.1	91813	42	AC010716	AC010716 Drosophil	c 907	16	1.1	112710	42	AC011252	AC011252 Drosophil
c 835	16	1.1	91863	8	ATAC004667	AC004667 Arabidops	c 908	16	1.1	112753	41	AC009459	AC009459 Drosophil
c 836	16	1.1	92472	10	HS181C9	Z98743 Human DNA s	909	16	1.1	112789	33	AL133341	AL133341 Homo sapi
c 837	16	1.1	92948	8	ATAF000657	AF000657 Arabidops	c 910	16	1.1	113220	42	AC009368	AC009368 Drosophil
c 838	16	1.1	93131	43	AC000105	AC000105 Homo sapi	911	16	1.1	113637	41	AC009765	AC009765 Homo sapi
c 839	16	1.1	93655	42	AC010559	AC010559 Drosophil	c 912	16	1.1	113687	40	AC005301	AC005301 Homo sapi
c 840	16	1.1	93845	8	ATAC004684	AC004684 Arabidops	913	16	1.1	114567	41	AC009417	AC009417 Homo sapi
c 841	16	1.1	94386	11	HS452M16	AL024493 Human DNA	914	16	1.1	115118	10	AP000247	AP000247 Homo sapi
c 842	16	1.1	96460	11	HS633O20	AL1023804 Human DNA	c 915	16	1.1	115319	43	AF202962	AF202962 Homo sapi
c 843	16	1.1	96679	8	HT8F19	AL133315 Arabidops	c 916	16	1.1	115907	33	HSJ651E10	AL122002 Homo sapi
c 844	16	1.1	96801	8	ATAC003033	AC003033 Arabidops	c 917	16	1.1	115962	41	AC008441	AC008441 Homo sapi
c 845	16	1.1	96924	45	AC017831	AC017831 Drosophil	c 918	16	1.1	116828	32	HSJ272H18	AL109826 Homo sapi
c 846	16	1.1	96953	41	AC011428	AC011428 Homo sapi	c 919	16	1.1	116868	42	AC010029	AC010029 Drosophil
c 847	16	1.1	97146	8	AC007259	AC007259 Arabidops	920	16	1.1	117896	42	AC010750	AC010750 Drosophil
c 848	16	1.1	97308	43	AC013925	AC013925 Drosophil	c 921	16	1.1	118067	10	HS163M9	AL021920 Homo sapi
c 849	16	1.1	97693	40	AC002383	AC002383 Homo sapi	922	16	1.1	118100	45	AC017911	AC017911 Drosophil
c 850	16	1.1	98052	10	AP000219	AP000219 Homo sapi	c 923	16	1.1	118235	12	AC003060	AC003060 Mus muscu
c 851	16	1.1	98052	10	AP000341	AP000341 Homo sapi	c 924	16	1.1	118831	11	HS989H11	283851 Human DNA s
c 852	16	1.1	98124	8	ATT161L	AL031394 Arabidops	c 925	16	1.1	119001	8	ATAC005896	AC005896 Arabidops
c 853	16	1.1	98695	35	AC005556	AC005556 Drosophil	c 926	16	1.1	119122	42	AC010003	AC010003 Drosophil
c 854	16	1.1	99346	8	AF076243	AF076243 Arabidops	927	16	1.1	119348	42	AC009369	AC009369 Drosophil
c 855	16	1.1	99416	8	AC009398	AC009398 Genomic s	c 928	16	1.1	119399	33	AC007757	AC007757 Drosophil
c 856	16	1.1	99856	8	ATF24G24	AL049488 Arabidops	c 929	16	1.1	119430	33	ATF9D16	AL035394 Arabidops
c 857	16	1.1	100000	9	AB020860	AB020860 Homo sapi	c 930	16	1.1	119751	33	AC007755	AC007755 Drosophil
c 858	16	1.1	100000	10	AP000040	AP000040 Homo sapi	c 931	16	1.1	122228	10	AC000003	AC000003 Homo sapi
c 859	16	1.1	100000	10	AP000069	AP000069 Homo sapi	932	16	1.1	123091	34	CEY87G2A	AL110500 Caenorhab

c 933	1.1	123360	10	HS222E13	293241 Human DNA s
c 934	1.1	123421	33	AC007756	AC007756 Drosophill
c 935	1.1	123551	33	AC005809	AC005809 Homo sapi
c 936	1.1	123737	41	AF189001	AF189001 Homo sapi
c 937	1.1	123947	40	AC005045	AC005045 Homo sapi
c 938	1.1	124539	33	AC008043	AC008043 Drosophill
c 939	1.1	125010	41	AC011394	AC011394 Homo sapi
c 940	1.1	125235	33	AC008197	AC008197 Drosophill
c 941	1.1	125368	42	AC008929	AC008929 Homo sapi
c 942	1.1	125729	11	HS971N18	AL021396 Human DNA
c 943	1.1	126356	33	AC006876	AC006876 Caenorhab
c 944	1.1	127168	10	HS1163J1	AL031588 Human DNA
c 945	1.1	127282	11	AC005155	AC005155 Homo sapi
c 946	1.1	127528	33	AC007821	AC007821 Drosophill
c 947	1.1	128150	8	AC007661	AC007661 Arabidops
c 948	1.1	128447	33	AC006849	AC006849 Drosophill
c 949	1.1	128598	1	D90912	D90912 Synchocyst
c 950	1.1	128765	40	HUAC002040	AC002040 Homo sapi
c 951	1.1	128992	33	HS223B1	AL031943 Homo sapi
c 952	1.1	129138	33	AC008205	AC008205 Drosophill
c 953	1.1	129191	42	AC009751	AC009751 Drosophill
c 954	1.1	129238	41	AC011469	AC011469 Homo sapi
c 955	1.1	129779	35	AC006214	AC006214 Drosophill
c 956	1.1	130142	45	AC017890	AC017890 Drosophill
c 957	1.1	130536	44	AC007807	AC007807 Drosophill
c 958	1.1	130583	41	AC007420	AC007420 Drosophill
c 959	1.1	130608	16	AF005370	AF005370 Alceiaphi
c 960	1.1	131024	33	AC004666	AC004666 Homo sapi
c 961	1.1	131410	44	AC008319	AC008319 Drosophill
c 962	1.1	131973	44	AF205589	AF205589 Homo sapi
c 963	1.1	132025	33	AC007824	AC007824 Drosophill
c 964	1.1	132418	33	AC006357	AC006357 Homo sapi
c 965	1.1	133772	43	AC010211	AC010211 Drosophill
c 966	1.1	134963	10	HS199L16	AL022151 Human DNA
c 967	1.1	135258	10	HS127B20	Z83838 Human DNA s
c 968	1.1	135296	42	AC010567	AC010567 Drosophill
c 969	1.1	135567	33	AC008235	AC008235 Drosophill
c 970	1.1	135648	11	AC004069	AC004069 Homo sapi
c 971	1.1	136145	41	AC008962	AC008962 Homo sapi
c 972	1.1	136200	33	AC008204	AC008204 Drosophill
c 973	1.1	136254	1	EC0UW82	L10328 E. coli; th
c 974	1.1	136742	1	ECUW82	U82598 Escherichia
c 975	1.1	136742	1	ECUW82598	U82598 Escherichia
c 976	1.1	136955	33	HS0306E2	AL121573 Homo sapi
c 977	1.1	137177	33	AC008189	AC008189 Drosophill
c 978	1.1	137654	32	AP000713	AP000713 Homo sapi
c 979	1.1	137974	42	AC010046	AC010046 Drosophill
c 980	1.1	138285	42	AC010047	AC010047 Drosophill
c 981	1.1	139415	42	AC012291	AC012291 Homo sapi
c 982	1.1	139480	43	AC012837	AC012837 Drosophill
c 983	1.1	139801	10	CNS01DS3	AL121653 BAC seque
c 984	1.1	139825	43	AC010919	AC010919 Drosophill
c 985	1.1	140331	40	AC007002	AC007002 Homo sapi
c 986	1.1	140942	10	AC002525	AC002525 Human PAC
c 987	1.1	141320	45	AC017833	AC017833 Drosophill
c 988	1.1	141744	1	ECU28377	U28377 Escherichia
c 989	1.1	142418	7	AF000815	AP000815 Oryza sat
c 990	1.1	142660	43	AC010968	AC010968 Homo sapi
c 991	1.1	142852	8	AF161269	AF161269 Oryza sat
c 992	1.1	143131	33	HS010739	AC007039 Homo sapi
c 993	1.1	143774	32	HSP10238	AC012239 Homo sapi
c 994	1.1	144673	43	AC012239	AC012239 Homo sapi
c 995	1.1	144720	41	AC009177	AC009177 Arabidops
c 996	1.1	145531	42	AC011180	AC011180 Homo sapi
c 997	1.1	146153	35	AC007452	AC007452 Drosophill
c 998	1.1	146458	33	AL133290	AL133290 Homo sapi
c 999	1.1	146497	33	AC007718	AC007718 Homo sapi
c 1000	1.1	146858	33	AC006457	AC006457 Homo sapi

RESULT 1

AG2H417/c

LOCUS AG2H417 91 bp DNA INV

DEFINITION A.gambiae satellite DNA (locus AG2H417).

ACCESSION 272082

VERSION 272082.1 GI:1292591

KEYWORDS satellite.

SOURCE African malaria mosquito.

ORGANISM Anopheles gambiae

REFERENCE 1 (bases 1 to 91)

AUTHORS Zheng, L., Benedict, M.O., Cornel, A.J., Collins, F.H. and Kafatos, F.C.

TITLE An integrated genetic map of the African human malaria vector mosquito, Anopheles gambiae

JOURNAL Genetics 143 (1996) In press

REFERENCE 2 (bases 1 to 91)

AUTHORS Zheng, L.

TITLE Direct Submission

JOURNAL Submitted (23-APR-1996) Zheng L., European Molecular Biology Laboratory, Meyerhofstrasse 1, 69117 Heidelberg, FRG

FEATURES

Location/Qualifiers

1..91

source

/organism="Anopheles gambiae"

/strain="Suakoko"

/db_xref="taxon:7165"

/chromosome="2"

/dev_stage="adult"

/clone_lib="phage M13"

/clone="PAG417"

/map="0 CM"

/note="polytene 7"

1..91

satellite

15 a 17 c 28 g 31 t

BASE COUNT

ORIGIN

Query Match 1.6%; Score 23; DB 34; Length 91;

Best Local Similarity 100.0%; Pred. No. 0.21;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1270 acccttcagacacataccgacag 1292

|||||

Db 64 ACCCTTCAGACATACCGACAG 42

RESULT 2

AG2H442/c

LOCUS AG2H442 93 bp DNA INV

DEFINITION A.gambiae satellite DNA (locus AG2H442).

ACCESSION 272084

VERSION 272084.1 GI:1292593

KEYWORDS satellite.

SOURCE African malaria mosquito.

ORGANISM Anopheles gambiae

REFERENCE 1 (bases 1 to 93)

AUTHORS Zheng, L., Benedict, M.O., Cornel, A.J., Collins, F.H. and Kafatos, F.C.

TITLE An integrated genetic map of the African human malaria vector mosquito, Anopheles gambiae

JOURNAL Genetics 143 (1996) In press

REFERENCE 2 (bases 1 to 93)

AUTHORS Zheng, L.

TITLE Direct Submission

JOURNAL Submitted (23-APR-1996) Zheng L., European Molecular Biology Laboratory, Meyerhofstrasse 1, 69117 Heidelberg, FRG

FEATURES

Location/Qualifiers

1..93

source

/organism="Anopheles gambiae"

/strain="Suakoko"

/db_xref="taxon:7165"

ALIGNMENTS

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/dev stage="adult"
/clone.lib="phage M13"
/clone="pac442"
/map="3.7 CM"
/note="polytene 7"
1. .93
/note="locus AG2H442"
BASE COUNT 15 a 20 c 28 g 30 t
ORIGIN

Query Match 1.6%; Score 23; DB 34; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1270 acccttcagacacatccagacag 1292
|||||
Db 62 ACCCTTCAGACACATACCGACAG 40

RESULT 3
GGU72352 1435 bp mRNA VRT 01-JUL-1997
LOCUS
DEFINITION Gallus gallus serine protease mRNA, partial cds.
ACCESSION U72352
VERSION U72352.1 GI:2228535
KEYWORDS
SOURCE chicken.
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 1435)
AUTHORS Kirby, M.L., Wallis, K.T., Rhodes, M.R., Stadt, H.A., Kumiski, D.H.,
Li, Y.X. and Lei, C.-L.
Direct Submission
Submitted (24-SEP-1996) Institute of Molecular Medicine and
Genetics, Medical College of Georgia, Laney Walker Blvd, Augusta,
GA 30912, USA
FEATURES
Source
1. .1435
/organism="Gallus gallus"
/strain="Arbor Acres"
/db_xref="taxon:9031"
/dev stage="embryo"
/tissue_type="neural crest"
<1. .1212
CDS
<1. .1212
/codon_start=1
/product="serine protease"
/protein_id="AA961899.1"
/db_xref="GI:2228536"
/translation="ARAPKGTATPAPVTSATPAGPRGTALWRHGGGALRRAR
RAGAGRCAMPSPPPGSPAAFNFIADYVEKTAFLVVEIVGRHPFSGREVPISN
RAGGLVSPDGLIVNAHVANRRVRVKLASGEQYDAVQDVQVADIAIRIKPKVR
AAAREGSLRLPSAYTVPLFQHPPLPTLPLGRSEVRQGVFWAMGSPFALQNTITSGI
YSSAQGRSLRLAASDMEXIQTDAIDFGNSGGLVNLDPGEVIGNTMTKVTSGISFA
IPSDRLKRFQKEERKSSWFGNAETKRRYIGVYMLLTLPQHPAEALKRDPSPDVSY
GVLIHKVIGSPAGLKGAGDVVLEINGQATRAEDVIEAVRIQQSLALLVRSYDT
LLVSVVPEVTE"
BASE COUNT 260 a 451 c 466 g 258 t
ORIGIN

Query Match 1.4%; Score 20; DB 4; Length 1435;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 817 ggcattctcttgccatccc 836
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Db 814 GGCATCTCTCTTGCCATCCC 833

RESULT 4
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```
GOGDH 2890 bp DNA
LOCUS
DEFINITION G.oxydans gdh gene.
ACCESSION X62710 S60040
VERSION X62710.1 GI:58416
KEYWORDS coenzyme PQQ; gdh gene; gluconic acid
dehydrogenase; quinoprotein.
SOURCE Gluconobacter oxydans.
ORGANISM Gluconobacter oxydans.
Bacteria; Proteobacteria; alpha subd.
Gluconobacter.
REFERENCE 1 (bases 1 to 2890)
AUTHORS Cleton-Jansen, A.M., Dekker, S., van de
TITLE A single amino acid substitution char
of quinoprotein glucose dehydrogenase in Gluconobacter oxydans
JOURNAL Mol. Gen. Genet. 229 (2), 206-212 (1991)
MEDLINE 92017653
REFERENCE 2 (bases 1 to 2890)
AUTHORS Goosen, N.
TITLE Direct Submission
JOURNAL Submitted (07-FEB-1992) N. Goosen, Dept of Mol Genetics, Gorlaeus
Laboratories, Leiden University, P O Box 9502, 2300 RA Leiden, THE
NETHERLANDS
FEATURES
Source
1. .2890
/organism="Gluconobacter oxydans"
/db_xref="taxon:442"
242. .245
251. .2677
/gene="gdh"
251. .2677
/gene="gdh"
/EC_number="1.1.99.17"
/codon_start=1
/transl_table=11
/product="glucose dehydrogenase
(pyroloquinoline-quinone)"
/protein_id="CAA44594.1"
/db_xref="GI:4493391"
/db_xref="SWISS-PROT:P27175"
/translation="MSTISRPRMLALITAAVFALCGAILTVGGAWAAAGGLPYVYL
GLALLATAFLSFRNPALYLFVAVFVGTIWEITVVGDLIDWALIPRSDIIVILGWL
LLPFVRSARSVARGRPSRPAVGAVLALFSLFDFPHDISGELPTQANASPADPD
NYPASEWHAYGRTQAGDRWPLNATVSNLKVAMHITKDMNSNDPGEATNEAT
PIEFNNTLYMCSLHOKLFAVDGATGVKVVYDPKLIQNFQHLTCRGVSFHTPANA
MSDGNPAPDCAKDSILPNDGRLVEVDATKTCGSGFNGEIDLRVFNQYPTTPG
QMETSPVITDKLIANSALTDNGSVKQASGATQAFDVTGKRVVVDASNDPQOL
PDSEHPVFPNSWISVSYDANLNLVTPMGVGTDPQWGDRTKDSERFAGIVAL
NADTGLAWFYQTVRHDLWMELPSQSLVDVTQKDGTLVPAIATPKTGDIIVLDRR
TGKEIVAPETVPVQGAAPGDHTSPTQPMSQLTRPKNPLNDSIDWGTIFDQMFCSI
YFHTLRVGEFTPPSLKGLIFPDGLGMEFWGLAVDPQVAFANPISLPFVSQLYVP
RGPGNPLMPREENAKGTGGTGLQHNIGIPYAVNLHPFLDPLVLPFGIKMPCPTPPWGY
VAGIDLKTKNVVQHNGLRDSMYGSSLPILPPIKIGVPSLGGPLSTAGNLGFLTA
SMDIYTRANLTTGKVLWQDRLPAGAQAIPITVAINKGQIVITYAGGHNSFPTRMGDD
IIAYALPDQK"
293. .664
/misc_feature /gene="gdh"
/note="membrane spanning fragment"
mutation 2612
/gene="gdh"
/note="mutation changing substrate specificity"
BASE COUNT 555 a 975 c 786 g 574 t
ORIGIN
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Query Match 1.4%; Score 20; DB 1; Length 2890;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

Qy 597 atgggtcgctgccatcgcg 616
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Db 340 ATGGGTCGCTGCCATCGCG 359
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```

RESULT 5
AC013843/c
LOCUS AC013843 31427 bp DNA HTG 16-NOV-1999
DEFINITION Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
pieces.
ACCESSION AC013843
VERSION AC013843.1 GI:6437492
KEYWORDS HTG; HTGS_PHASE2.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 31427)
AUTHORS Adams,M. and Venter,J.C.
JOURNAL Direct Submission
TITLES Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
COMMENT This sequence was identified as CDM:10211866 by the submitter.
For further information on this sequence e-mail to fly@celera.com.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
FEATURES
source
Location/Qualifiers
1..31427
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
BASE COUNT 8828 a 5834 c 6605 g 9160 t
ORIGIN

Query Match 1.4%; Score 20; DB 43; Length 31427;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 344 aagaagacgagatgacggc 363
|||||
Db 6506 AAGAAGACGACGATGCGC 6487

RESULT 6
AC005052
LOCUS AC005052 144734 bp DNA HTG 12-JUN-1998
DEFINITION Homo sapiens clone RG038K21, *** SEQUENCING IN PROGRESS ***, 3
unordered pieces.
ACCESSION AC005052
VERSION AC005052.1 GI:3212939
KEYWORDS HTG; HTGS_PHASE1.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 144734)
AUTHORS Waterston,R.H.
TITLES The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 144734)
AUTHORS Waterston,R.H.
TITLES Direct Submission
JOURNAL Submitted (12-JUN-1998) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 12548: contig of 12548 bp in length

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* 12549 12565: gap of unknown length
* 12566 66999: contig of 54434 bp in length
* 67000 67016: gap of unknown length
* 67017 144734: contig of 77718 bp in length.
FEATURES
Location/Qualifiers
1..144734
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RG038K21"
BASE COUNT 37035 a 34072 c 33954 g 39639 t 34 others
ORIGIN

Query Match 1.4%; Score 20; DB 33; Length 144734;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 673 agctgcccaacgaagccta 692
|||||
Db 84680 AGCTGCCCAACGAAGCTA 84699

RESULT 7
HTLV1RES
LOCUS HTLV1RES 2153 bp DNA PRI 24-JUN-1998
DEFINITION Human HTLV-I related endogenous retroviral sequence (HRES-1/1).
ACCESSION X16660
VERSION X16660.1 GI:3256208
KEYWORDS endogenous retrovirus; long terminal repeat.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2153)
AUTHORS Perl,A.
TITLES Direct Submission
JOURNAL Submitted (23-AUG-1989) Perl A., Roswell Park Memorial Institute,
666 Elm Street, Buffalo, NY 14263, USA
REMARK revised by [3]
REFERENCE 2 (bases 1 to 2153)
AUTHORS Perl,A., Rosenblatt,J.D., Chen,I.S., Divincenzo,J.P., Bever,R.,
Polesz,B.J. and Abraham,G.N.
TITLES Detection and cloning of new HTLV-related endogenous sequences in
man
JOURNAL Nucleic Acids Res. 17 (17), 6841-6854 (1989)
MEDLINE 89386040
REFERENCE 3 (bases 1 to 2153)
AUTHORS Perl,A.
TITLES Direct Submission
JOURNAL Submitted (23-JUN-1998) Perl A., Roswell Park Memorial Institute,
666 Elm Street, Buffalo, NY 14263, USA
COMMENT On Jun 26, 1998 this sequence version replaced gi:38034.
Data kindly reviewed (08-JAN-1990) by Perl A.
FEATURES
Location/Qualifiers
1..2153
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="T lymphocyte"
/cell_line="MA-T"
/clone_lib="lambda DASH"
/clone="HRES-1/1"
310..994
/notes="putative retroviral"
repeat_unit 310..313
/notes="A"
misc_feature 463..470
/pt_type=INVERTED
TATA_signal 782..788
misc_feature 839..844
/notes="putative"
repeat_unit 990..993
/notes="A"
LTR

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[illegible]

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SISVLINGESTGKSLVAHALHRHSPRSKAPFIALNMAAIKDLIESELFGHEKGAFT
GANTYGRFQADGGTFLDEIGMDPLDVTQTLRLRLVLDAGQFYRVGGYAPVKVDVRI
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BASE COUNT 994 a 1199 c 1150 g 973 t
ORIGIN

Query Match 1.4%; Score 19; DB 2; Length 4316;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1230 acagcaatccggtacgcttc 1248
|||||
DB 272 ACAGCAATCCGCTACGCTTC 254

RESULT 9
AF067430/c
LOCUS AF067430 6417 bp DNA ROD 05-OCT-1999
DEFINITION Mus musculus Smarcel-related protein (Smarcelr) gene, complete cds.
ACCESSION AF067430
VERSION AF067430.1 GI:4321967
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 6417)
Wattler,F., Wattler,S., Kelly,M., Skinner,H.B. and Nehls,M.
Cloning, chromosomal location, and expression analysis of murine
Smarcel-related, a new member of the high-mobility 365 group gene
family

JOURNAL Genomics 60 (2), 172-178 (1999)

MEDLINE 99417677

REFERENCE 2 (bases 1 to 6417)

AUTHORS Wattler,S., Wattler,F. and Nehls,M.

TITLE Direct Submission

JOURNAL Submitted (20-MAY-1998) New Technologies, Lexicon Genetics Inc.,
4000 Research Forest Drive, The Woodlands, Texas 77381, USA

FEATURES Location/Qualifiers

source

1. .6417
/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="10"
/map="43 cm"

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2128..2295,2773..2845,3225..3440,3589..3721,3804..4230)

/gene="Smarcelr"

/product="Smarcel-related protein"

270..4230

/gene="Smarcelr"

/note="similar to Mus musculus Baf57 and other Smarcel
genes"

CDS Join(573..610,1256..1364,1655..1858,2128..2295,2773..2845,
3225..3440,3589..3721,3804..3816)

/gene="Smarcelr"

/note="contains HMG domain and kinesin-like coiled-coil
domain; SWI/SNF related, matrix associated, actin
dependent regulator of chromatin subfamily E, member
1-related protein"

/codon_start=1

/product="Smarcel-related protein"

/protein_id="AA015897.1"

/db_xref="GI:4321968"

/translation="MSHGPRPGPAATAGGKTPQHGAFVAVVAVKQERSEGRAGEKG
PQEEPRVKRGPKGKKKTLIPNGKAPVTGYRFLNERQEIETRPDLPFPFETIK
MLGAWSKLQPAEKQYLDIAEKEKQYLKWYQQSEAYKVKTEKIQENKIKEDS
SSGLMNTLLNHGKGVDCGFSTFDVPIETFEFLDQNKAREALRLRKNVAFERQNA
VLQRTQMSARLERLEGLALEERTLALQQLQQAVALTASPASLPVPGTGETPT
LGTLDYMARLHGATERDPAQHERLIARVKELARVASEHL"

polyA_site
4209..4214

/gene="Smarcelr"
BASE COUNT 1394 a 1863 c 1788 g 1372 t
ORIGIN

Query Match 1.4%; Score 19; DB 12; Length 6417;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 217 gtagcccccgcgcgcgcgcga 235
|||||
DB 382 GCAGCCCCGCGCCCGCGCA 364

RESULT 10
CELTI14F9

LOCUS CELTI14F9 36679 bp DNA INV 04-MAR-1996

DEFINITION Caenorhabditis elegans cosmid T14F9.

ACCESSION U50199

VERSION U50199.1 GI:1213552

KEYWORDS

SOURCE Caenorhabditis elegans strain-Bristol N2.

ORGANISM Caenorhabditis elegans

REFERENCE 1 (bases 1 to 36679)
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

AUTHORS

Wilson,R., Ainscough,R., Anderson,K., Baynes,C., Berks,M.,
Bonfield,J., Burton,J., Connell,M., Copsey,T., Cooper,J.,
Coulson,A., Craxton,M., Dear,S., Du,Z., Durbin,R., Favello,A.,
Fulton,L., Gardner,A., Green,P., Hawkins,T., Hillier,L., Jier,M.,
Johnston,L., Jones,M., Kershaw,J., Kirsten,J., Laister,N.,
Latrelle,P., Lightning,J., Lloyd,C., McMurray,A., Mortimore,B.,
O'Callaghan,M., Parsons,J., Percy,C., Rifen,L., Roopra,A.,
Saunders,D., Showkneen,R., Smaildon,N., Smith,A., Sonhammer,E.,
Staden,R., Sulston,J., Thierry-Mieg,J., Thomas,K., Vaudin,M.,
Vaughan,K., Waterston,R., Watson,A., Weinstock,L.,
Wilkinson-Sproat,J. and Wohldman,P.

2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans

JOURNAL Nature 368 (6466), 32-38 (1994)

MEDLINE 94150718

REFERENCE 2 (bases 1 to 36679)

AUTHORS Miller,N and Langston,Y.

TITLE The sequence of C. elegans cosmid T14F9

JOURNAL Unpublished (1996)

REFERENCE 3 (bases 1 to 36679)

AUTHORS Waterston,R.

TITLE Direct Submission

JOURNAL Submitted (28-FEB-1996) Robert Waterston

COMMENT Submitted by:

Genome Sequencing Center
Department of Genetics, Washington University,
St. Louis, MO 63110, USA, and
Sanger Centre, Hinxton Hall
Cambridge CB10 1RQ, England
e-mail: rwhematode.wustl.edu and jess@sanger.ac.uk

NEIGHBORING COSMID INFORMATION:

The 5' cosmid is T24C12, 200 bp overlap;3' cosmid is F07D10, 200 bp
overlap. Actual start of this cosmid is at base position 197 of
CELTI14F9; actual end is at 36483 of CELTI14F9
The poly-G run from 8005 to 8024 may be off by one G. An exact
number could not be determined.

NOTES:

Coding sequences below are predicted from computer analysis, using
the program Genefinder(P. Green and L. Hillier, ms in preparation).

FEATURES

source

1..36679

/organism="Caenorhabditis elegans"

/strain="Bristol N2"

/db_xref="taxon:6239"

8005..8024

/note="Poly G run"

repeat_region

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12342. .12929,12984. .13085)
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/evidence=not_experimental
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/db_xref="GI:1213553"
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RNPDIQIVTSFGYQKLYGYRINIQIAPERNFKSRVCYCAKKHWDGOWCKCRA
ETMDNKNACKSHNPPRRHVAEIEFKSOLYSAALENPDHGDGLVNOASWYLSL
GYMFENKSKSLVARNKDGKPKPKRSKRMKFEVDDDDENKMKPLETDSCEL
PFINNVKPEPESHPTIQTPOIPTIHOQQEQSNLLQAPATLNGMNNPWGMEH
LAMIWAANMLPGDLVSLTAALSCKHOQHVGOPSPQAAATPTASISNLSVSFT
POMPKASATAPLOQLVNLKDLKPLPLANTQTSPIVQAANLLPVAALKDSSTQT
TEIKVSOCLTSGCGGRVIRICCCDEGVCRRTAAC"
18470. .21495
/gene="T14F9.3"
join(18470. .18568,18613. .18739,18793. .18918,18964. .19079,
19421. .19633,19677. .19907,19952. .20127,20175. .20435,
20477. .20599,21300. .21495)
/gene="T14F9.3"
/notes="coded for by C. elegans cDNA yk79c7.3; coded for by
C. elegans cDNA yk79c7.5; Similar to beta-hexosaminidase
beta subunit."
/codon_start=1
/protein_id="AAA91263.1"
/db_xref="GI:1213554"
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DECPGPPVAGSEYLLRSLTEAVINAQTVMGALRAMESLSHLVYDHKSQEIQR
TVEIFDPFVRGIMIDSSRHFLSVNVIKRLQELMSKMLNVLHVLHSDSEFPYTS
VKFPELHGAGVSPRHVYSREDIADIAFAKRLGIRVPEIDLPGLTSSWRGKGLT
ECFKEKMEKFGNDVLENYFEKLYKIVENLKKRKLFWOEVDENINIPDN
AVIHWGNTHEEYEQVKNTITSONFVIVSACVNLNRYIGADWRDEIRGTAPSNSR
YIICDPTFNFTGTAQELVWGVIAGIWCGLVNTNIEARLWPRASAAELWSPAEKT
QRAEDAWPRMHELRCRLVSRGYRIQPNPNPDYCPFEDEPPATKTEL"
complement(22182. .22253)
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complement(24191. .24790)
/gene="lin-32"
complement(join(24191. .24337,24722. .24790))
/gene="lin-32"
/notes="T14F9.5"
/codon_start=1
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/db_xref="GI:1213555"
/translation="MRRSAANERERRRMTNLNVADELREVLPEIDSGKLSKETLQ
MAQYIECLSQILKQDSKNENLKSQG"
28980. .31448
/gene="T14F9.2"
join(28980. .28988,29309. .29409,29462. .29866,29912. .30036,
30082. .30254,30301. .30420,31194. .31448)
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/codon_start=1
/evidence=not_experimental
/protein_id="AAA91265.1"
/db_xref="GI:1213556"
/translation="MTGMSSEDQAPNGSVPGDPAKAWPELTVDLEPVRALYRKH
GERFCRSEMLMELEIESCEIAEQKLLDILVKVTFIERNLCLNGPQSGESLSELE
ARSDQPLFATVSDLSFCDSMRPIQTEKVKGTLLVRSNGYSRRFIQYIRRLPE
GDVIDSTFRQVIOFQDTIGVPDSVFFKASELTLDFTSLRVARNVPGFYDKSLSE
RLDLPTEAEHLHLPLFTFTLDFNPNHDKDYSFVSCVYRNDCTOYPRNLKTVYS
TPGLGIGMFCQDNKMDYLGNDLEKGTFFNAARYFLAPEGNINRSNLSEYEFVKVYN
ITFGFDNLLVTGNTIYRVHFNLEKVDSTFENVQTELEATLRVRVHRTKSKEDNDN
SDD"
32897. .34887
/gene="T14F9.1"
join(32897. .32977,33031. .33126,33181. .33321,33370. .33483,
33533. .33640,33689. .34183,34448. .34650,34713. .34887)

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/notes="coded for by C. elegans cDNA yk89e9.5; coded for by
C. elegans cDNA cm795; coded for by C. elegans cDNA
cm1499; coded for by C. elegans cDNA yk52g5.5; coded for
by C. elegans cDNA yk76e5.5; coded for by C. elegans cDNA
yk131f11.5; coded for by C. elegans cDNA yk87d8.5; coded
for by C. elegans cDNA yk76e5.3; coded for by C. elegans
cDNA CEESU78FB; coded for by C. elegans cDNA yk52g5.3; coded for by C.
elegans cDNA yk131f11.3; similar to S. cerevisiae
vacuolar H(+)-ATPase 54 kd subunit (SP:P41807)"
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/db_xref="GI:1213557"
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DMLOEKSRVSEFLKQKNTNDYMTTARCFQKMLRHDHIEHFVDSQGVPLVTAL
EGDLOQYVSEFLKQKNTNDYMTTARCFQKMLRHDHIEHFVDSQGVPLVTAL
NGKTFLOXOLIFAVYKTFNADIAKAPSLGILQALGDILSESEKVRIRILASF
VNLISKVDREVEREALQVOKTLLKTLMDAKYDDPDLEKVFLEETLSVH
DLSYDEYIYSEVRSGRLQSPVHSEKFWENAKSKFNQKQFVYVYKILKLESHDPL
ILCVASHDIEGYVHRHPRKIVVEYQGRKAAVMRLLTAEADPNVRYHALLAQVLMVHN
WEYLKQLDSDVQDTTAVAK"
11140 a 7051 c 6678 g 11810 t
BASE COUNT
ORIGIN
Query Match 1.4%; Score 19; DB 34; Length 36679;
Best Local Similarity 100.0%; Pred. No. 42; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0;
QY 619 cccttcgcttgacaca 637
|||||
Db 31266 CCCTTCGCTTTCGACACA 31284
RESULT 11
SPBC2F12 38012 bp DNA PLN 23-NOV-1999
LOCUS S. pombe chromosome II cosmid c2F12.
DEFINITION 297211
ACCESSION 297211.2 GI:6273683
VERSION 60s ribosomal protein L22; atf creb-family transcription factor;
KEYWORDS byr2; bz1P; bz1P transcription factor; cegl; cell cycle regulation;
ergosterol synthesis; Homol D box; Homol E box; IMP dehydrogenase;
inosine-5'-monophosphate dehydrogenase; kinesin-like; L2; L8;
leucine zipper; mitochondrial 60s ribosomal protein L17; mitotic
cell cycle start; mrna capping enzyme; mrna guanylyltransferase;
rep2; rpk37; rpk5b; rpk5c; rpl17; rpl8-2; serine rich; serine
threonine protein kinase; transcriptional activator; zinc finger
C2H2 type.
fission yeast.
Schizosaccharomyces pombe
Schizosaccharomycetes
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales;
Schizosaccharomycetaceae; Schizosaccharomycetes.
1 (bases 1 to 38012)
Wood, V., Rajandream, M.A., Barrell, B.G., Skelton, J. and
Churcher, C.M.
Direct Submission
Submitted (27-JUN-1997) European Schizosaccharomycetes genome
sequencing project, Sanger Centre, The Wellcome Trust Genome
Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrellesanger.ac.uk
and The Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA
On Nov 7, 1999 this sequence version replaced gi:2239231.
Notes:
Details of yeast sequencing at the Sanger Centre are available on
the World Wide Web.
(URL, http://www.sanger.ac.uk/projects/S_pombe/)
During 1995 to 1996 about 80% of S. pombe chromosome 1 was
sequenced by the Sanger Centre. The sequencing of the S. pombe
genome is now being continued with funding from the European
Commission. Fourteen European sequencing laboratories, including

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the Sanger Centre, are participating in the project.

Protein coding regions (CDS) have been predicted with the help of computer analysis using the Genefinder program in Pombase (an ACEDB database) with additional predictions for the branch-acceptor sites supplied by the program Splice. CAUTION: It is possible that for any individual CDS we may have underestimated or overestimated the number of introns/exons or we may not have chosen the correct splice donor/acceptor sites.

CDS are numbered using the following system eg SPBC25H2.01c. SP (S. pombe), B (chromosome 2), c25H2 (cosmid name), .01 (first CDS), c (complementary strand).

The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous.

The length in codons is given for each CDS.

IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.

Cosmid c2F12 is overlapped at the 5' end by cosmid c19C2 and at the 3' end by cosmid cid7.

FEATURES

```

source
    location/Qualifiers
    1..38012
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    /strain="972h-"
    /db_xref="taxon:4896"
    /chromosome="II"
    /clone="cosmid c2F12"
    /map="IIR"
    misc_feature
    1..789
    /note="nominal overlap with cosmid SPBC19C2, EM:AL109731
    S.pombe chromosome 2"
    complement(1..371)
    /gene="SPBC2F12.16"
    CDS
    complement(join(1..308,359..371))
    /partial
    /gene="SPBC2F12.16"
    /note="SPBC2F12.16, similarity: to C elegans
    O17040, r15B7.2 PROTEIN, (271 aa), fasta scores, opt:135,
    E():2.7e-06, (36.8% identity in 87 aa overlap)"
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    /protein_id="CAB10163.2"
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    /db_xref="SWISS-PROT:O14346"
    /translation="MSKILKIQYLLKLYNVISCFLLMWSVLLRTGLIWGITKDTAVFHE
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    YLSMT"
    complement(309..327)
    /gene="SPBC2F12.16"
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    complement(353..358)
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    /note="taaga, splice donor sequence"
    1008..2069
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    join(1008..1235,1308..2069)
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    /note="SPBC2F12.15c, len:329aa; similarity: to YNL326C,
    YN6_6_YEAST, P42836, hypothetical 39.2 kd protein,
    (336aa), fas ta scores, opt:340, E():2.7e-1, (33.2%
    identity in 217 aa overlap)"
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    FVAIPKTTAGCANISALYLVFWGLFAFVGMSIVMTAFYFHTSLIHLNLSLESM
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misc_feature
1236..1241
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/note="gtacgt, splice donor sequence"
1290..1307
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/note="ctaactctctgtttcag, splice branch and acceptor"
3582..3588
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join(3582..4038,4371..5488)
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/note="SPBC2F12.14c, len:524aa, similarity: to IMH2_YEAST,
P50095, probable inosine-5'-monophosphate dehydrogenase
(523aa), fasta scores, opt:2200, E():0, (62.8% identity
in 524 aa overlap)"
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TPERQAAMVRKVKYENGFIIDPVVFSPOHTVGDLVLTKEIKGSGIITENGKLRGK
LVGIVTSRDVGFHKTDTNPTVEVTPREELITTAEGISLERANEMLRKSQKGLPVVD
KDDNLVALLSLTDLKMLHFFPLASKTSOTKQLMVAALIGTRDDOKTRJALAEAGLDA
VVIDSSQNSCFQIEMIKWIKTKYPRIDVIAGNVVTRQTAASLAAGADGLRUGMSG
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GGLLAGTTESPGEYVVRGQYKSYRGMSIAAMEGTGVNKNASTGRVFSENDAVRVA
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/note="Confirmed intron"
4039..4044
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/note="gtaagt, splice donor sequence"
4208..4288
/gene="SPBC2F12.14c"
/note="putative snRNA Sp-snr54, complements: Sp-18S-rRNA
and modifies Am989. Yeast snr54 homolog. (Todd Lowe)"
4360..4370
/gene="SPBC2F12.14c"
/note="ctaacttttag, splice branch and acceptor"
4463..4621
/gene="SPBC2F12.14c"
/note="Match to PF00571 CBS, CBS domain Score 46.07"
4715..5380
/gene="SPBC2F12.14c"
/note="Match to PF00478 IMPDH_C, IMP dehydrogenase / GMP
reductase C terminus Score 363.99"
complement(5821..8528)
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complement(join(5821..8441,8498..8528))
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YGM6_YEAST, P53086, putative kinesin-like protein,
(803aa), fas ta scores, opt:1347, E():0, (39.0% identity in
731 aa overlap)"
/codon_start=1
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PGLIYLTUKLEFMRMDHURDEKIFDLRLSYLEIVNETIDLLVSPTPNOAKPLNRED
ADRRITVPLGLTSLSPESLEEIIDIMKGNANRMTSPTAANAASSRSSHVAQVTLQKP

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BASE COUNT 25991 a 21189 c 20209 g 26030 t
ORIGIN /chromosomes="X"

Query Match 1.4%; Score 19; DB 32; Length 93419;
Best Local Similarity 100.0%; Pred.No.43;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 810 attcatgggcatctctctt 828
|||||
Db 4421 ATTCATGGCATCTCTCTT 4439

RESULT 14
MUSTHREX17/c
LOCUS MUSTHREX17 247 bp DNA ROD 18-OCT-1994
DEFINITION Mouse thrombospondin (THBS1) gene, exon 17.
ACCESSION M62465 S79284
VERSION M62465.1 GI:202015
KEYWORDS glycoprotein; thrombospondin.
SEGMENT 17 of 22
SOURCE Mus musculus (strain BALB/c, sub_species domesticus) DNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Lawler J., Duquette M., Ferro P., Copeland N.G., Gilbert D.J. and
Jenkins N.A.
TITLE Characterization of the murine thrombospondin gene
JOURNAL Genomics 11 (3), 587-600 (1991)
MEDLINE 92128941
FEATURES
source Location/Qualifiers
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/strain="BALB/c"
/sub_species="domesticus"
/db_xref="taxon:10090"
intron <1..6
/gene="THBS1"
/number=16
exon 7..241
/gene="THBS1"
/number=17
intron 242..>247
/gene="THBS1"
/number=17

BASE COUNT 73 a 64 c 64 g 46 t
ORIGIN

Query Match 1.3%; Score 18; DB 12; Length 247;
Best Local Similarity 100.0%; Pred.No.1.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 817 ggcattctcttgccatc 834
|||||
Db 153 GGCATCTCTCTTGCCATC 136

RESULT 15
G14673/c
LOCUS G14673 400 bp DNA STS 04-JAN-1996
DEFINITION human STS SHGC-11830.
ACCESSION G14673
VERSION G14673.1 GI:1130412
KEYWORDS STS sequence; primer; sequence tagged site.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Euthera; Archonta; Primates;
Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 400)
AUTHORS Myers,R.M.
JOURNAL Unpublished (1995)
COMMENT
Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259687
Fax: 4157259689
Email: myers@shgc.stanford.edu
Primer A: CTAGGAAACCATTTGTCAGCC
Primer B: GTCTCAATTGTTGACGCTTATCC
PCR Profile:
Initial incubation: 94 degrees C for 90 seconds
Denaturation: 94 degrees C for 15 seconds
Annealing: 62 degrees C for 23 seconds
Polymerization: 72 degrees C for 30 seconds
PCR Cycles: 30
Thermal Cycler: Perkin Elmer 9600
Protocol:
Template: 25 ng
Primer: each 1 uM
dNTPs: each 200 uM
Taq Polymerase: 0.05 units/ul
Total Vol: 10 ul
Buffer: MgCl2: 2.5 mM
KCl: 50 mM
Tris-HCl: 20 mM
pH: 8.3

Prepared with primer pairs derived from T62818--Merck/Uniest.
FEATURES
source Location/Qualifiers
1..400
/organism="Homo sapiens"
STS 121..251
primer_bind 121..142
primer_bind complement(229..251)
BASE COUNT 113 a 85 c 88 g 114 t
ORIGIN

Query Match 1.3%; Score 18; DB 13; Length 400;
Best Local Similarity 100.0%; Pred.No.1.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1266 cattacccttcagacaca 1283
|||||
Db 357 CATTACCCTTCAGACACA 340
Search completed: April 14, 2000, 18:33:06
Job time: 8214 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2000, 18:29:32 ; Search time 121.06 Seconds
(without alignments)
2883.016 Million cell updates/sec

Title: US-09-388-090-3
Perfect score: 1395
Sequence: 1 gtgttcaaaaataccaata.....tcagggaagtcctccgtcaa 1395

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 311585 seqs, 125096042 residues

Word size : 0
Total number of hits satisfying chosen parameters: 623170

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Listing first 1000 summaries

Database : N_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	1.3	965	X13598	Enterococcus faec
2	18	1.3	9960	V58939	Mycobacterium smeg
3	18	1.3	10095	V58938	Mycobacterium tube
4	17	1.2	196	T19263	Human gene signatu
5	17	1.2	229	V31989	BS106 polynucleoti
6	17	1.2	308	V31990	BS106 polynucleoti
7	17	1.2	482	V31992	Human secreted pro
8	17	1.2	489	X00704	Human secreted pro
9	17	1.2	489	X00644	BS106 polynucleoti
10	17	1.2	553	V31993	Human secreted pro
11	17	1.2	732	V29521	Homo sapiens Lexa-
12	17	1.2	1029	V28875	Candida antarctica
13	17	1.2	1348	V84576	Human secreted pro
14	17	1.2	1503	V29523	Homo sapiens PSP1
15	17	1.2	1787	V29522	Homo sapiens PSP1
16	17	1.2	1803	V24135	Homo sapiens BAP28
17	17	1.2	1835	V29524	Homo sapiens PSP1
18	17	1.2	2040	V08860	Human cancer-relat
19	17	1.2	2144	V29538	Homo sapiens PSP1-
20	17	1.2	2187	V29535	Homo sapiens PSP1-
21	17	1.2	2187	V29536	Homo sapiens PSP1-
22	17	1.2	2187	V29539	Homo sapiens PSP1-
23	17	1.2	2551	V29537	The soraphen biosy
24	17	1.2	49377	V05287	Staphylococcus aur
25	16	1.1	334	V75215	Rat allograft infl
26	16	1.1	388	Q99376	Staphylococcus aur
27	16	1.1	588	X07117	Mutant farnesylidp
28	16	1.1	894	T40228	Papaya ringspot vi
29	16	1.1	918	T38731	Papaya ringspot vi
30	16	1.1	926	X40028	Prostate cancer as
31	16	1.1	929	T38329	Coat protein gene
32	16	1.1	1080	X14364	H. pylori GHPO 376
33	16	1.1	1148	T71230	Papaya ringspot vi

34	16	1.1	1158	1	T34672
35	16	1.1	1288	1	Q36841
c 36	16	1.1	1479	1	T77329
c 37	16	1.1	1479	1	T93796
c 38	16	1.1	1479	1	V58021
39	16	1.1	2061	1	Q76669
40	16	1.1	2157	1	Q25801
41	16	1.1	2157	1	Q54772
42	16	1.1	2157	1	V59844
43	16	1.1	3710	1	V74716
44	16	1.1	4190	1	V34854
c 45	16	1.1	4426	1	V09064
c 46	16	1.1	4474	1	Q79703
c 47	16	1.1	4841	1	T05696
c 48	16	1.1	4968	1	X20597
c 49	16	1.1	5541	1	Q55755
50	16	1.1	7900	1	X13068
51	16	1.1	8378	1	Q25811
c 52	16	1.1	9432	1	Q99312
53	16	1.1	10461	1	X20553
54	16	1.1	11907	1	Q45339
55	16	1.1	13256	1	X20528
c 56	16	1.1	13811	1	X20649
57	16	1.1	14255	1	Q43526
58	16	1.1	14255	1	Q75181
59	16	1.1	14255	1	V20477
60	16	1.1	52297	1	T51411
61	16	1.1	52298	1	Q47357
62	15	1.1	47	1	V45614
63	15	1.1	54	1	V70987
c 64	15	1.1	247	1	X11700
c 65	15	1.1	247	1	X11701
c 66	15	1.1	247	1	X12866
c 67	15	1.1	288	1	X41498
c 68	15	1.1	307	1	T00043
c 69	15	1.1	345	1	T60544
c 70	15	1.1	383	1	X39585
c 71	15	1.1	409	1	V75474
c 72	15	1.1	417	1	T60542
c 73	15	1.1	438	1	T57431
74	15	1.1	448	1	V38433
75	15	1.1	493	1	Q59843
c 76	15	1.1	550	1	V63932
77	15	1.1	570	1	Q27165
78	15	1.1	573	1	Q36018
79	15	1.1	573	1	X23714
80	15	1.1	597	1	X3715
81	15	1.1	622	1	T98746
c 82	15	1.1	642	1	V23478
83	15	1.1	662	1	T83942
84	15	1.1	662	1	V53386
85	15	1.1	766	1	X23719
86	15	1.1	795	1	T00051
87	15	1.1	804	1	T70089
88	15	1.1	807	1	X02185
89	15	1.1	811	1	Q22605
c 90	15	1.1	865	1	V58741
91	15	1.1	1000	1	V27350
92	15	1.1	1074	1	X12946
c 93	15	1.1	1102	1	X23720
c 94	15	1.1	1126	1	V58744
95	15	1.1	1139	1	V08813
96	15	1.1	1290	1	T67838
97	15	1.1	1290	1	X30416
98	15	1.1	1308	1	Q14367
99	15	1.1	1341	1	V29071
c 100	15	1.1	1367	1	X51727
101	15	1.1	1371	1	T29383
c 102	15	1.1	1434	1	T72221
103	15	1.1	1438	1	X23317
104	15	1.1	1482	1	Q05236
c 105	15	1.1	1650	1	T04376
c 106	15	1.1	1662	1	T62457

Coat protein gene
Cyclophilin C: Cyc
Class II EPSPS DNA
Class II EPSP synt
Dichelobacter nodo
Variant cyclomalto
H13 gene. Human re
Full-length human
Human retroviral r
Staphylococcus aur
Human retinal dege
Bovine GMP-bindin
Cyclic guanosine m
Flax rust resistan
Polynucleotide seq
Escherichia coli g
Enterococcus faeca
Drosophila SLIR pr
LKPI operon. Haemo
Polynucleotide seq
cDNA encoding htrx
Polynucleotide seq
Polynucleotide seq
ALL-1 gene cDNA. D
ALL-1 (acute lymph
Human ALL-1/AF-4 o
Mycobacteriophage
I5 mycobacterioph
Primer for Mycobac
Primer 5'PRAC used
Human biallelic po
Human biallelic po
Human biallelic po
Human secreted pro
Hepatitis GB virus
{Pro23-Lys37}delasn
Human secreted pro
Staphylococcus aur
MetGDNF degenerate
H. pylori secreted
cDNA encoding the
Human brain Expres
Mycobacterium tube
Mink growth hormon
Gene for mink grow
Pig growth hormone
Pig growth hormone
DNA encoding a S.
Pseudomonas Xcp p s
DNA encoding a sin
DNA encoding a sin
Hepatitis GB virus
DNA encoding inter
E. coli dsbG DNA.
Mink pre-growth ho
Insertion sequence
Streptococcus pneu
Pig growth hormone
Enterococcus faeca
Insertion sequence
Gene No. 3 encodin
H. pylori secreted
H. pylori cell env
Citrate synthase g
Mycobacterium tube
DNA encoding a hum
Hamster flank orga
Grapevine leafroll
Human 1-alpha-OHAs
Glucose-6-phosphat
Moraxella catarrha
Streptomyces venez

c 107	1.1	1700	1	T90097	Mch4 coding sequen	c 180	15	1.1	5006	1	T61381	Parathyroid calciu
c 108	1.1	1704	1	V18819	Human protease FMH	c 181	15	1.1	5006	1	T95838	Human parathyroid
c 109	1.1	1763	1	T36360	Bst DNA polymerase	c 182	15	1.1	5006	1	T26963	Human parathyroid
c 110	1.1	1764	1	T90819	Bacillus stearothe	c 183	15	1.1	5006	1	V82484	Human parathyroid
c 111	1.1	1767	1	T98669	Sequence encoding	c 184	15	1.1	5125	1	T09703	IRS-1. Purified nu
c 112	1.1	1770	1	T98020	B. steatothermophi	c 185	15	1.1	5169	1	T06001	Streptomyces wedmo
c 113	1.1	1788	1	V71036	mpKAc-green floure	c 186	15	1.1	5238	1	V55846	GTPase activating
c 114	1.1	1938	1	Q31987	Heat stable hydant	c 187	15	1.1	5275	1	T95857	Bovine parathyroid
c 115	1.1	1946	1	V80304	Human GILR protein	c 188	15	1.1	5275	1	V26962	Bovine parathyroid
c 116	1.1	1966	1	X04340	Human secreted pro	c 189	15	1.1	5275	1	V82483	Bovine parathyroid
c 117	1.1	1988	1	Q20590	Sequence of native	c 190	15	1.1	5309	1	Q10280	Complete sequence
c 118	1.1	2019	1	T15007	Type III (alpha-ty	c 191	15	1.1	5448	1	V65229	DNA encoding a S.
c 119	1.1	2021	1	Q79725	Human L5/3 tumour	c 192	15	1.1	6256	1	T31299	Rice Xa21 disease
c 120	1.1	2021	1	T62438	Human L5/3 partial	c 193	15	1.1	6399	1	X13013	Enterococcus faeca
c 121	1.1	2040	1	T59913	Yeast transcriptio	c 194	15	1.1	6469	1	Q11690	Entire sequence of
c 122	1.1	2062	1	V44862	Clone BV291_3 codi	c 195	15	1.1	6469	1	X11294	Enterococcus faeca
c 123	1.1	2082	1	V41257	Mouse neuronal PAS	c 196	15	1.1	7204	1	X23527	O. longistaminta X
c 124	1.1	2092	1	T14529	Human adenyl cycl	c 197	15	1.1	7451	1	V05856	Complete sequence
c 125	1.1	2100	1	V82073	DNA encoding gidA	c 198	15	1.1	7571	1	V52135	Streptococcus pneu
c 126	1.1	2116	1	T99541	Human hyaluronan s	c 199	15	1.1	7664	1	X13312	Enterococcus faeca
c 127	1.1	2117	1	T96713	Human hyaluronate	c 200	15	1.1	8051	1	T72685	Sugar biosynthesis
c 128	1.1	2152	1	V26613	Human LiCE3 cDNA.	c 201	15	1.1	8160	1	X25774	S. erythraea erythr
c 129	1.1	2161	1	Q98671	Sequence encoding	c 202	15	1.1	8169	1	V26609	Actinomadura hibis
c 130	1.1	2180	1	Q20589	Sequence of PCR-ge	c 203	15	1.1	9271	1	V23080	Fragment HGJ2141 o
c 131	1.1	2213	1	T47149	Macrophage stimula	c 204	15	1.1	9395	1	V76930	GT10 gene cDNA se
c 132	1.1	2216	1	T47145	Macrophage stimula	c 205	15	1.1	9408	1	V68336	Human BAZ2-alpha c
c 133	1.1	2216	1	V72083	Human MSP cDNA. Tr	c 206	15	1.1	9493	1	T00129	Human BAZ2-alpha c
c 134	1.1	2219	1	Q79723	Human L5/3 tumour	c 207	15	1.1	9493	1	T59784	Streptococcus pneu
c 135	1.1	2219	1	Q79724	Human L5/3 tumour	c 208	15	1.1	10708	1	V69286	FHA structural gen
c 136	1.1	2219	1	T62437	Human L5/3 partial	c 209	15	1.1	10820	1	X20537	Streptococcus pneu
c 137	1.1	2219	1	T62436	Human L5/3 partial	c 210	15	1.1	10974	1	V52347	Polynucleotide seq
c 138	1.1	2262	1	Q79729	Full-length human	c 211	15	1.1	12036	1	Q04688	Streptococcus pneu
c 139	1.1	2262	1	T62439	Human L5/3 constru	c 212	15	1.1	12665	1	V52267	Streptococcus pneu
c 140	1.1	2325	1	T04156	Enzyme Q36 coding	c 213	15	1.1	13154	1	X13275	Enterococcus faeca
c 141	1.1	2352	1	V20575	Human pro-tumour n	c 214	15	1.1	13340	1	X23522	O. longistaminta
c 142	1.1	2352	1	V73948	Human TNF-alpha co	c 215	15	1.1	13811	1	X20649	Polynucleotide seq
c 143	1.1	2355	1	V80664	Human DNAX toll-i	c 216	15	1.1	14051	1	V74414	Staphylococcus aur
c 144	1.1	2376	1	V72590	Mouse neurotropsin	c 217	15	1.1	17378	1	X20510	Polynucleotide seq
c 145	1.1	2471	1	T58548	Bacillus lichenifo	c 218	15	1.1	17612	1	V23494	Polynucleotide seq
c 146	1.1	2614	1	X19027	Mouse serine prote	c 219	15	1.1	19142	1	X20580	Pseudomonas Xpc, O
c 147	1.1	2640	1	T22790	Clas I S-receptor	c 220	15	1.1	19446	1	V52184	Polynucleotide seq
c 148	1.1	2717	1	Q23504	Pectin-lyase-I gen	c 221	15	1.1	19639	1	X23524	Streptococcus pneu
c 149	1.1	2749	1	Q63492	S-Locus receptor (c 222	15	1.1	22191	1	X20600	O. longistaminta
c 150	1.1	2780	1	X13729	Brassica sp. S-rec	c 223	15	1.1	31517	1	X20600	Polynucleotide seq
c 151	1.1	2880	1	X13729	Rat VRL capsidin	c 224	15	1.1	49272	1	V35000	Enterococcus faeca
c 152	1.1	3073	1	T04158	Enzyme Q36 coding	c 225	15	1.1	53526	1	T94101	Mycobacteriophage
c 153	1.1	3098	1	Q36363	Defective tyrosine	c 226	15	1.1	53577	1	T18551	Human PKD1 gene. H
c 154	1.1	3098	1	Q70808	Protein kinase (HR	c 227	15	1.1	53577	1	T94108	Human polycystic k
c 155	1.1	3098	1	Q92943	Saccharomyces cere	c 228	15	1.1	53577	1	V30458_1	Human PKD1 locus b
c 156	1.1	3125	1	N70455	5'-3' sequence of	c 229	15	1.1	110000	1	V21209_00	Continuation (2 of
c 157	1.1	3150	1	V74654	Staphylococcus aur	c 230	15	1.1	110000	1	V21209_03	Methanococcus jann
c 158	1.1	3305	1	Q39967	PKC-alpha cDNA. Ne	c 231	15	1.1	110000	1	V21209_12	Continuation (4 of
c 159	1.1	3372	1	N80755	Encodes all HAV st	c 232	15	1.1	110000	1	V21209_14	Continuation (13 of
c 160	1.1	3384	1	T86165	Nucleotide sequenc	c 233	15	1.1	110000	1	V30459_1	Continuation (15 of
c 161	1.1	3627	1	V08574	CSB2 coding sequen	c 234	15	1.1	134525	1	Q04525	Continuation (2 of
c 162	1.1	3684	1	V15222	Bacillus thuringie	c 235	14	1.0	20	1	Q28443	Total base sequenc
c 163	1.1	3809	1	T61382	Parathyroid calciu	c 236	14	1.0	21	1	T01684	HIV-1 ribozyme #1.
c 164	1.1	3809	1	T95859	Human parathyroid	c 237	14	1.0	21	1	T11998	Peptide nucleic ac
c 165	1.1	3809	1	V26964	Human parathyroid	c 238	14	1.0	21	1	X17915	CMV antisense olig
c 166	1.1	3809	1	V82485	Human parathyroid	c 239	14	1.0	27	1	Q30207	Anti-CMV oligonuc
c 167	1.1	3921	1	T31300	Rice Xa21 disease	c 240	14	1.0	27	1	V98185	HCV-US anti-sense
c 168	1.1	4086	1	Q51033	Human myoD gene an	c 241	14	1.0	29	1	V93242	Human EGF-R hamme
c 169	1.1	4131	1	T89290	Dogfish shark kidn	c 242	14	1.0	32	1	V00369	Human B-raf hamme
c 170	1.1	4131	1	T95860	Rat kidney cell ca	c 243	14	1.0	36	1	T54406	Bacillus thuringie
c 171	1.1	4131	1	V26965	Rat kidney calcium	c 244	14	1.0	40	1	Q88332	Human IL-5 hamme
c 172	1.1	4131	1	V82486	Rat parathyroid ca	c 245	14	1.0	46	1	X22931	Maize alpha-tubuli
c 173	1.1	4185	1	V52306	Streptococcus pneu	c 246	14	1.0	46	1	X22925	DE19736591 primer
c 174	1.1	4219	1	V74523	Staphylococcus aur	c 247	14	1.0	54	1	X48756	DE19736591 primer
c 175	1.1	4359	1	V40711	Aldehyde oxidase g	c 248	14	1.0	125	1	X12672	TDH (52-78) primer
c 176	1.1	4412	1	V40710	Aldehyde oxidase g	c 249	14	1.0	129	1	X10430	Human biallelic po
c 177	1.1	4440	1	T68322	Human multidrug re	c 250	14	1.0	141	1	V76149	Human biallelic po
c 178	1.1	4602	1	V59574	Human secreted pro	c 251	14	1.0	153	1	V75664	Staphylococcus aur
c 179	1.1	4879	1	V74400	Staphylococcus aur	c 252	14	1.0	159	1	Q65715	CMP-NeuAc hydroxyl

c 253	14	1.0	159	1	T40843	Serine protease nf	326	14	1.0	391	1	V89105	EST clone BX141. N
254	14	1.0	166	1	T22272	Human gene signatu	327	14	1.0	396	1	N90326	Hepatitis C virus
255	14	1.0	177	1	T43883	Mutated human immu	328	14	1.0	396	1	N92096	Sequence of the he
256	14	1.0	177	1	T27788	Mutated human immu	329	14	1.0	400	1	X40927	Human secreted pro
c 257	14	1.0	195	1	T67548	H. pylori secreted	c 329	14	1.0	402	1	V70394	Nucleic acid seque
258	14	1.0	198	1	T24785	H. pylori ORF 06ep	331	14	1.0	408	1	Q68187	Sequence encoding
259	14	1.0	200	1	X39511	Human secreted pro	332	14	1.0	408	1	Q84033	PMON5853 encodes (
c 260	14	1.0	215	1	V76480	Staphylococcus aur	333	14	1.0	408	1	Q95148	Human interleukin-
c 261	14	1.0	219	1	Q43595	Synthetic pTHLP ge	334	14	1.0	409	1	V86576	EST clone AW106. N
262	14	1.0	240	1	Q11971	RaIT scorpion toxi	335	14	1.0	414	1	Q68188	Sequence encoding
c 263	14	1.0	252	1	T67640	H. pylori secreted	c 336	14	1.0	414	1	Q84005	PMON5853 encodes (
c 264	14	1.0	259	1	T23925	Human gene signatu	337	14	1.0	419	1	T30730	Mouse cryptidin 5 g
c 265	14	1.0	271	1	T23925	Modified kringle d	c 338	14	1.0	419	1	T47254	(DSM 10104) human
c 266	14	1.0	271	1	Q04648	Staphylococcus aur	c 339	14	1.0	420	1	X24811	Hypersensitive res
c 267	14	1.0	271	1	V75308	Human gene signatu	340	14	1.0	421	1	T30743	Mouse cryptidin 5 c
c 268	14	1.0	274	1	T25165	Human gene signatu	341	14	1.0	422	1	T26471	Human gene signatu
c 269	14	1.0	297	1	T25681	Human gene signatu	342	14	1.0	429	1	T68026	H. pylori secreted
c 270	14	1.0	303	1	V89591	EST clone CN951. N	343	14	1.0	430	1	V90253	EST clone D1516. N
271	14	1.0	315	1	Q84029	PMON5974 encodes (c 344	14	1.0	443	1	Q05206	Primer binding to
272	14	1.0	317	1	V90674	Nucleotide sequenc	345	14	1.0	461	1	X34704	DNA sequence of mo
273	14	1.0	321	1	Q59801	Human brain Expres	346	14	1.0	479	1	Q37619	Vdelta2 (cell line
274	14	1.0	321	1	V90720	Nucleotide sequenc	c 347	14	1.0	485	1	V34604	Mycobacterium vacc
275	14	1.0	333	1	T27924	PRLTS gene exon 2	c 348	14	1.0	485	1	V34570	M. vaccae antigen
276	14	1.0	333	1	T27167	PRLTS coding seque	349	14	1.0	486	1	T70120	Clone C-11-3 from
277	14	1.0	330	1	Q84025	PMON5968 encodes (350	14	1.0	511	1	V69351	Rice glycogenin cl
c 278	14	1.0	331	1	V87021	EST clone BG142. N	351	14	1.0	515	1	X21179	Polynucleotide seq
279	14	1.0	332	1	Q68095	Sequence encoding	c 352	14	1.0	523	1	Q56098	Probe for Cryptosp
280	14	1.0	333	1	Q68102	Sequence encoding	353	14	1.0	526	1	V84494	Human secreted pro
281	14	1.0	333	1	Q68096	Sequence encoding	c 354	14	1.0	536	1	X13610	Enterococcus faeca
282	14	1.0	333	1	Q68104	Sequence encoding	c 355	14	1.0	540	1	N70767	Sequence of the na
283	14	1.0	333	1	Q68097	Sequence encoding	356	14	1.0	556	1	Q37621	Vdelta3 (cell line
284	14	1.0	333	1	Q68103	Sequence encoding	357	14	1.0	556	1	Q37618	Vdelta2 (cell line
285	14	1.0	333	1	Q68093	Sequence encoding	c 358	14	1.0	568	1	Q84670	Yeast presuence
286	14	1.0	333	1	Q68098	Sequence encoding	c 359	14	1.0	568	1	Q70273	Yeast presuence
287	14	1.0	333	1	Q68099	Sequence encoding	c 360	14	1.0	576	1	T67669	H. pylori cell env
288	14	1.0	336	1	Q84007	PMON5901 encodes (c 361	14	1.0	583	1	T60819	Guanylate cyclase
289	14	1.0	336	1	Q84009	PMON5901 encodes (c 362	14	1.0	583	1	T65115	Human GCAP-II prec
290	14	1.0	336	1	Q84010	PMON5969 encodes (363	14	1.0	602	1	T58577	Cryptosporidium pa
291	14	1.0	336	1	Q84011	PMON5976 encodes (c 364	14	1.0	624	1	N71272	Sequence of adult
292	14	1.0	336	1	Q84012	PMON5941 encodes (c 365	14	1.0	644	1	N60396	Sequence of promot
293	14	1.0	336	1	Q84013	PMON5976 encodes (366	14	1.0	647	1	Q73017	Hepatitis Type-C v
294	14	1.0	336	1	Q84013	PMON5941 encodes (c 367	14	1.0	648	1	Q67257	Silver fox growth
295	14	1.0	336	1	Q84014	PMON5961 encodes (c 368	14	1.0	657	1	X54627	Human IL-3 recepto
296	14	1.0	336	1	Q84021	PMON5960 encodes (369	14	1.0	657	1	T47185	HTLV-I gp24 gag ge
297	14	1.0	336	1	Q84022	PMON5961 encodes (c 370	14	1.0	675	1	V26689	Human novel secret
298	14	1.0	336	1	Q84023	PMON5962 encodes (371	14	1.0	687	1	T41495	DNA encoding MAGe-
299	14	1.0	336	1	Q84024	PMON5970 encodes (c 372	14	1.0	695	1	V53471	Clone encoding a Sta
300	14	1.0	336	1	Q84027	PMON5972 encodes (373	14	1.0	705	1	T38006	Clone MSRV2SPR iso
301	14	1.0	336	1	Q84027	PMON5973 encodes (c 374	14	1.0	711	1	X34231	Mycobacterium spec
302	14	1.0	336	1	Q84030	PMON5975 encodes (c 375	14	1.0	712	1	V27391	Streptococcus pneu
303	14	1.0	336	1	Q84031	PMON5977 encodes (c 376	14	1.0	714	1	V75009	Staphylococcus aur
304	14	1.0	339	1	Q68081	Sequence of plasm	377	14	1.0	717	1	X22939	Chlamydomonas sp.
305	14	1.0	339	1	Q68082	Sequence encoding	c 378	14	1.0	721	1	V84605	Human secreted pro
306	14	1.0	339	1	Q68185	Sequence encoding	379	14	1.0	723	1	T86281	Soybean albumin 1
307	14	1.0	339	1	Q68184	Sequence encoding	c 380	14	1.0	723	1	V65275	DNA encoding a S.
308	14	1.0	339	1	Q68110	Sequence encoding	c 381	14	1.0	738	1	N70037	Insulin-like growt
309	14	1.0	339	1	Q68108	Sequence encoding	382	14	1.0	748	1	T02826	Multiple sclerosis
310	14	1.0	339	1	Q68109	Sequence encoding	383	14	1.0	748	1	T38004	Clone MSRV-2EL1. D
311	14	1.0	339	1	Q84015	PMON5978 encodes (384	14	1.0	748	1	V43126	Multiple sclerosis
312	14	1.0	339	1	Q84016	PMON5978 encodes (385	14	1.0	753	1	T67487	H. pylori surface
313	14	1.0	339	1	Q84017	PMON5967 encodes (c 386	14	1.0	759	1	V04597	Flea serine protea
314	14	1.0	339	1	Q84032	PMON5980 encodes (387	14	1.0	762	1	T73988	Sequence 40 from W
315	14	1.0	340	1	Q68186	Sequence encoding	388	14	1.0	762	1	V23289	Synthetic green fl
316	14	1.0	342	1	Q84020	PMON5979 encodes (389	14	1.0	772	1	X20015	Enterococcus faeca
317	14	1.0	345	1	Q61337	Human brain Expres	390	14	1.0	774	1	Q92407	Human cyclin A pro
c 318	14	1.0	359	1	T75248	Nucleotide sequenc	391	14	1.0	780	1	Q67206	Canine growth horm
319	14	1.0	360	1	Q84004	PMON5853 encodes (392	14	1.0	780	1	Q67207	Gly184, Ala186-Can
320	14	1.0	360	1	Q84006	PMON5872 encodes (393	14	1.0	783	1	Q66887	Human lymphocyte c
321	14	1.0	361	1	T26578	Human gene signatu	394	14	1.0	798	1	T88156	E. coli fish autotr
322	14	1.0	362	1	V20261	Probe (162) for mi	395	14	1.0	800	1	X16086	DNA encoding wild-
323	14	1.0	378	1	Q84068	PMON5887 encodes (c 396	14	1.0	801	1	X13673	Enterococcus faeca
c 324	14	1.0	381	1	T33511	Infectious laryngo	397	14	1.0	801	1	T68280	H. pylori putative
325	14	1.0	384	1	V86069	EST clone D14. New	398	14	1.0	805	1	X18954	Fructose:glucose r

C 399	14	1.0	807	1	Q98735	Barley Ltp2 gene p	472	14	1.0	1247	1	Q45120	Human GDF-1(fx) mo
C 400	14	1.0	828	1	T68075	H. pylori secreted	473	14	1.0	1247	1	Q67402	Human GDF-1(fx) mo
C 401	14	1.0	839	1	V34717	Human Fancoi I CD	474	14	1.0	1247	1	T97883	CDNA sequence enco
C 402	14	1.0	840	1	X20014	Enterococcus faeca	475	14	1.0	1247	1	V10351	Human GDF-1 CDNA.
C 403	14	1.0	845	1	T66947	Chicken interleuki	476	14	1.0	1247	1	V19538	Human GDF-1 (fx) p
C 404	14	1.0	850	1	T40855	Serine protease nf	477	14	1.0	1247	1	V32588	Human GDF-1 CDNA.
C 405	14	1.0	857	1	V75197	Staphylococcus aur	478	14	1.0	1254	1	Q10952	Insert from pigl e
C 406	14	1.0	858	1	V45175	Human LEA-motif de	c 479	14	1.0	1255	1	T13981	Human body weight
C 407	14	1.0	861	1	V43021	Streptococcus pneu	c 480	14	1.0	1255	1	V09078	Human C5 gene CDNA
C 408	14	1.0	867	1	T74471	Open reading frame	c 481	14	1.0	1266	1	X25773	S.erythraea erythr
C 409	14	1.0	879	1	T01341	Human FK506 bindin	c 482	14	1.0	1268	1	Q26713	Encodes exon I of
C 410	14	1.0	884	1	N70391	Human recombinant	c 483	14	1.0	1275	1	V59143	Phaffia rhodozyma
C 411	14	1.0	891	1	N70036	Insulin-like growt	c 484	14	1.0	1280	1	Q51487	CDNA encoding orn
C 412	14	1.0	897	1	V24697	H. pylori ORF 14ae	485	14	1.0	1290	1	Q03061	Human T-cell leuke
C 413	14	1.0	912	1	V46315	Human secreted pro	486	14	1.0	1306	1	V52019	Helicobacter poly
C 414	14	1.0	913	1	Q70048	Diofilaria immiti	c 487	14	1.0	1307	1	Q31804	Brassica thioester
C 415	14	1.0	925	1	T15611	CROC-4 CDNA encode	c 488	14	1.0	1307	1	Q65407	Brassica campestr
C 416	14	1.0	925	1	V16740	CDNA encoding huma	c 489	14	1.0	1307	1	Q92309	Brassica acyl thio
C 417	14	1.0	940	1	X21054	Polynucleotide seq	c 490	14	1.0	1307	1	V15236	Brassica campestr
C 418	14	1.0	945	1	V90853	Nucleotide sequenc	c 491	14	1.0	1314	1	T51410	Human ribosomal pr
C 419	14	1.0	945	1	X25733	B.subtilis cystein	492	14	1.0	1315	1	Q22997	Human 2p3 gene. Hu
C 420	14	1.0	950	1	Q11972	Scorpion toxin exp	c 493	14	1.0	1328	1	Q94882	Barley Ltp2 gene.
C 421	14	1.0	954	1	X20092	Enterococcus faeca	494	14	1.0	1329	1	V71080	Green fluorescent
C 422	14	1.0	963	1	V55148	Multi-functional h	495	14	1.0	1333	1	V05317	Mouse haematopoiet
C 423	14	1.0	963	1	V55150	Multi-functional h	c 496	14	1.0	1335	1	T47875	K. pneumoniae alco
C 424	14	1.0	971	1	X37469	Human secreted pro	497	14	1.0	1338	1	Q99004	Canine cholecystok
C 425	14	1.0	972	1	T34189	PopD coding sequen	498	14	1.0	1338	1	T10093	Canine cholecystok
C 426	14	1.0	972	1	V55149	Multi-functional h	499	14	1.0	1338	1	T15959	Canine cholecystok
C 427	14	1.0	972	1	V55151	Multi-functional h	500	14	1.0	1343	1	T98589	Canine cholecystok
C 428	14	1.0	981	1	V12756	A. faecalis JM3 ni	c 501	14	1.0	1347	1	T41699	ONC encoding a S.
C 429	14	1.0	981	1	X16591	Helicobacter pylor	c 502	14	1.0	1356	1	T42060	Onchocerca volvulu
C 430	14	1.0	1001	1	X20478	Human secreted pro	503	14	1.0	1357	1	T66555	Bovine rotavirus v
C 431	14	1.0	1004	1	X13479	Enterococcus faeca	504	14	1.0	1383	1	T42055	Rabies virus nucle
C 432	14	1.0	1023	1	V24931	H. pylori cell env	c 505	14	1.0	1386	1	V59647	Kurthia sp. biotin
C 433	14	1.0	1027	1	X13585	Enterococcus faeca	c 506	14	1.0	1389	1	V21235	Homo sapiens clone
C 434	14	1.0	1023	1	X34232	Myobacterium spec	507	14	1.0	1399	1	X20017	Enterococcus faeca
C 435	14	1.0	1025	1	V18441	Unknown DNA sequen	c 508	14	1.0	1416	1	X30587	H. pylori outer me
C 436	14	1.0	1034	1	X14407	H. pylori GHPO 604	c 509	14	1.0	1434	1	X16007	DNA encoding an an
C 437	14	1.0	1068	1	X13571	Enterococcus faeca	c 510	14	1.0	1435	1	X14025	H. pylori GHPO 525
C 438	14	1.0	1083	1	T14024	Drosophila dCREB2-	c 511	14	1.0	1437	1	Q36687	Sequence encoding
C 439	14	1.0	1095	1	V99747	IL-1 alpha propiec	c 512	14	1.0	1437	1	Q48234	Cytochrome C gene.
C 440	14	1.0	1097	1	V44860	Clone BG142.1 codi	c 513	14	1.0	1437	1	T71594	Myobacterium tube
C 441	14	1.0	1101	1	V25033	H. pylori cell env	c 514	14	1.0	1437	1	V29069	Myobacterium tube
C 442	14	1.0	1101	1	V25034	H. pylori cell env	c 515	14	1.0	1437	1	V42598	M. tuberculosis 56
C 443	14	1.0	1103	1	V05139	CDNA encoding mur	516	14	1.0	1440	1	Q47998	Sequence encoding
C 444	14	1.0	1110	1	V24662	H. pylori ORF 05gp	517	14	1.0	1440	1	V74943	Staphylococcus aur
C 445	14	1.0	1115	1	V48115	Nucleotide sequenc	518	14	1.0	1448	1	T84017	DNA encoding a sul
C 446	14	1.0	1116	1	V25108	H. pylori ORF 06ap	519	14	1.0	1448	1	V53413	DNA encoding a sir
C 447	14	1.0	1125	1	N91423	Sequence of heat-r	520	14	1.0	1450	1	Q98003	Canine cholecystok
C 448	14	1.0	1125	1	Q70705	Plasmin receptor D	521	14	1.0	1450	1	T10092	Canine cholecystok
C 449	14	1.0	1125	1	T67935	H. pylori cytoplas	c 522	14	1.0	1463	1	V00123	Rat hexokinase enc
C 450	14	1.0	1127	1	V12757	A. faecalis JM3 ni	c 523	14	1.0	1488	1	X03981	Thermus flavus TE3
C 451	14	1.0	1138	1	V46314	Human secreted pro	c 524	14	1.0	1493	1	V01889	Human OTK27 gene.
C 452	14	1.0	1140	1	V71081	Alpha-actinin acti	525	14	1.0	1500	1	X20016	Enterococcus faeca
C 453	14	1.0	1143	1	T34428	Eucalyptus AGE1 CD	526	14	1.0	1508	1	T37312	Aromatic acyl tran
C 454	14	1.0	1187	1	V74711	Staphylococcus aur	527	14	1.0	1509	1	V24861	H. pylori secreted
C 455	14	1.0	1200	1	Q05728	Gene encoding glut	528	14	1.0	1509	1	V24959	H. pylori secreted
C 456	14	1.0	1200	1	V24539	Full length mouse	529	14	1.0	1512	1	Q14274	Chimpanzee HCV clo
C 457	14	1.0	1200	1	V74138	Mouse FLAME-2 CDNA	530	14	1.0	1512	1	Q73003	Hepatitis Type C v
C 458	14	1.0	1204	1	X14194	H. pylori GHPO 885	531	14	1.0	1512	1	Q98204	Hepatitis C virus
C 459	14	1.0	1204	1	X14194	H. pylori GHPO 169	532	14	1.0	1512	1	V70801	Insert of a HCV cl
C 460	14	1.0	1221	1	X30447	H. pylori outer me	533	14	1.0	1512	1	V70547	Insert of a HCV cl
C 461	14	1.0	1224	1	T15858	Canine cholecystok	534	14	1.0	1513	1	X14006	H. pylori GHPO 144
C 462	14	1.0	1224	1	T67867	H. pylori cell env	535	14	1.0	1513	1	Q22988	Sequence of the SA
C 463	14	1.0	1236	1	Q58033	TRP-1 promoter. DN	536	14	1.0	1517	1	Q25268	Protease inhibitor
C 464	14	1.0	1238	1	Q70537	Nicotinamide aden	537	14	1.0	1523	1	Q91523	Soluble murine Mpl
C 465	14	1.0	1239	1	T68012	H. pylori secreted	c 538	14	1.0	1529	1	Q88328	Maize alpha-tubuli
C 466	14	1.0	1239	1	X07132	Staphylococcus aur	539	14	1.0	1530	1	N50275	Sequence from PATK
C 467	14	1.0	1239	1	X07112	Staphylococcus aur	c 540	14	1.0	1539	1	T17153	Myobacterium tube
C 468	14	1.0	1247	1	Q41354	Human GDF-1 coding	c 541	14	1.0	1548	1	Q13868	Insert from clone
C 469	14	1.0	1247	1	Q38862	Morphogen GDF-1 co	c 542	14	1.0	1552	1	T72713	Drosophila inhibit
C 470	14	1.0	1247	1	Q58055	Human morphogenic	543	14	1.0	1558	1	Q27988	Protease from S. A
C 471	14	1.0	1247	1	Q67315	Human GDF-1(fx) mo	544	14	1.0	1560	1	V72221	Autographa califor

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c 545	14	1.0	1576	1	Q10226	Clone pGEM-hBARGam	618	14	1.0	1839	1	Q29147	DNA encoding p34 f
546	14	1.0	1584	1	V84358	Streptococcus pneu	c 619	14	1.0	1839	1	Q29147	DNA encoding p34 f
547	14	1.0	1586	1	Q27987	Protease from S. A	c 620	14	1.0	1842	1	T68244	H. pylori inner me
548	14	1.0	1587	1	X13606	Enterococcus faeca	c 621	14	1.0	1845	1	V25052	H. pylori cell env
c 549	14	1.0	1592	1	V44638	Human uncoupling p	c 622	14	1.0	1851	1	Q38249	HCV CKS-ENV recomb
c 550	14	1.0	1596	1	V82381	Full length human	c 623	14	1.0	1851	1	Q38264	HCV CKS-ENV recomb
c 551	14	1.0	1597	1	V43827	Atrazine chlorohyd	c 624	14	1.0	1851	1	Q38279	Mutant lipase codi
c 552	14	1.0	1599	1	V38531	DNA marker of meta	c 625	14	1.0	1851	1	X27845	PHCV-104 - recomb
553	14	1.0	1600	1	Q85770	Low affinity nerve	c 626	14	1.0	1854	1	Q21691	CDNA encoding chlm
554	14	1.0	1602	1	Q72217	Human adrenergic r	c 627	14	1.0	1862	1	Q46007	CDNA encoding the pr
555	14	1.0	1605	1	V72222	Baculovirus ISP DN	c 628	14	1.0	1863	1	N60399	Sequence of the pr
c 556	14	1.0	1611	1	V21655	AAV4 Rep 68 gene.	c 629	14	1.0	1865	1	V41728	Endotoxin Crya(c)
c 557	14	1.0	1612	1	V44595	Human respiration	c 630	14	1.0	1868	1	T59712	Carrot reverse tra
c 558	14	1.0	1620	1	Q00543	Vampire bat plasm	c 631	14	1.0	1872	1	Q35220	AAV4 Rep gene. Ade
c 559	14	1.0	1630	1	N70315	Sequence encoding	c 632	14	1.0	1872	1	V21649	AAV4 Rep 78 gene.
c 560	14	1.0	1630	1	X14097	H. pylori GPPO 137	c 633	14	1.0	1872	1	V21649	BUF-3 gene for hum
c 561	14	1.0	1631	1	V44636	Human uncoupling p	c 634	14	1.0	1873	1	Q01648	Arp 4 gene. New Sc
c 562	14	1.0	1633	1	V43824	Atrazine chlorohyd	c 635	14	1.0	1886	1	Q04453	Sequence encoding
c 563	14	1.0	1635	1	V71073	CDK2-green fluores	c 636	14	1.0	1886	1	Q05966	Human alpha lc adr
c 564	14	1.0	1635	1	V71074	Green fluorescent	c 637	14	1.0	1890	1	Q89781	Jnk1-green floures
c 565	14	1.0	1667	1	V52050	Helicobacter polyp	c 638	14	1.0	1893	1	V71033	Jnk1-green floures
c 566	14	1.0	1689	1	T08083	Alpha-1,3/4-fucosi	c 639	14	1.0	1896	1	V71022	Jnk1-green floures
c 567	14	1.0	1721	1	T39752	Macaque mucosal ad	c 640	14	1.0	1902	1	V71118	Encodes human Reti
c 568	14	1.0	1724	1	T40082	M. tuberculosis RN	c 641	14	1.0	1903	1	Q10389	Human retinoic aci
c 569	14	1.0	1735	1	T77840	Human melanoma ass	c 642	14	1.0	1905	1	N90395	Genomic/CDNA compo
c 570	14	1.0	1738	1	T98569	DNA encoding a S.	c 643	14	1.0	1906	1	N70306	Sequence encoding
c 571	14	1.0	1739	1	T74472	Open reading frame	c 644	14	1.0	1906	1	Q92784	Mullerian inhibiti
c 572	14	1.0	1757	1	Q49428	Cytochrome P450 ho	c 645	14	1.0	1907	1	X20307	Borrelia burgdorfe
c 573	14	1.0	1757	1	T94866	Petunia flavonoid	c 646	14	1.0	1908	1	V71079	Green fluorescent
c 574	14	1.0	1758	1	N90600	CDNA encoding huma	c 648	14	1.0	1919	1	Q11055	Clone 19 encoding
c 575	14	1.0	1758	1	Q04719	Sequence encoding	c 649	14	1.0	1926	1	Q79624	DNA encoding malol
c 576	14	1.0	1758	1	Q06099	DNA encoding human	c 650	14	1.0	1929	1	V58275	Fluorescent calmod
c 577	14	1.0	1758	1	Q20201	Human serum albumi	c 651	14	1.0	1929	1	V58277	Fluorescent calmod
c 578	14	1.0	1758	1	T75084	Human serum albumi	c 652	14	1.0	1934	1	V45793	Heliothis ecodyson
c 579	14	1.0	1761	1	T12919	Human serum albumi	c 653	14	1.0	1940	1	V41732	DNA encoding a for
c 580	14	1.0	1761	1	T12920	Human serum albumi	c 654	14	1.0	1942	1	Q37616	TCR delta protein
c 581	14	1.0	1761	1	V07282	Human semaphorin W	c 655	14	1.0	1942	1	V58276	Fluorescent calmod
c 582	14	1.0	1763	1	T12918	Human serum albumi	c 656	14	1.0	1958	1	V58276	Human HFGAN72 rece
c 583	14	1.0	1765	1	T12921	Human serum albumi	c 657	14	1.0	1959	1	T85095	Human HFGAN72 rece
c 584	14	1.0	1767	1	T12922	Human serum albumi	c 658	14	1.0	1971	1	V28138	Fluorescent calmod
c 585	14	1.0	1770	1	Q79692	HCY RNA-dependent	c 659	14	1.0	1971	1	Q72212	Truncated human al
c 586	14	1.0	1770	1	T63432	Bacillus caldotena	c 660	14	1.0	1983	1	V24954	H. pylori inner me
c 587	14	1.0	1779	1	Q31651	Saccharomyces cere	c 661	14	1.0	1983	1	V24954	H. pylori ORF 06ep
c 588	14	1.0	1779	1	T85394	DNA encoding matur	c 662	14	1.0	1986	1	T48588	cDNA coding for CM
c 589	14	1.0	1782	1	N90128	Sequence of protei	c 663	14	1.0	1986	1	T78596	Cytidine monophosp
c 590	14	1.0	1784	1	N40163	Sequence of protei	c 664	14	1.0	1987	1	T11624	Human truncated al
c 591	14	1.0	1784	1	N40145	Murine ikaros gene	c 665	14	1.0	1988	1	V80364	Human homeobox gen
c 592	14	1.0	1788	1	Q44979	Murine ikaros CDNA	c 666	14	1.0	1988	1	T11600	Human alpha-1C adr
c 593	14	1.0	1788	1	T63431	Hepatitis C virus	c 667	14	1.0	1997	1	T11600	Human alpha-1C adr
c 594	14	1.0	1788	1	V66968	Murine ikaros enco	c 668	14	1.0	1998	1	Q72213	Human melanoma ass
c 595	14	1.0	1788	1	V42805	Murine ikaros isofo	c 669	14	1.0	2000	1	T77839	Human secreted pro
c 596	14	1.0	1788	1	V07920	Helicobacter pylor	c 670	14	1.0	2003	1	V84571	Human alpha-1C adr
c 597	14	1.0	1799	1	X18925	Phaseolus lunatus	c 671	14	1.0	2004	1	T11599	H. pylori cell env
c 598	14	1.0	1812	1	Q70903	Cold acclimatizati	c 672	14	1.0	2004	1	V25065	Human alpha-1C adr
c 599	14	1.0	1813	1	N70309	Sequence of bovine	c 673	14	1.0	2005	1	Q27211	Human alpha-1C adr
c 600	14	1.0	1814	1	X04373	Human secreted pro	c 674	14	1.0	2007	1	Q27287	DNA encoding TAP.
c 601	14	1.0	1814	1	V71031	Erk2-green floures	c 675	14	1.0	2007	1	V25147	H. pylori cell env
c 602	14	1.0	1815	1	V71023	Green flourescent	c 676	14	1.0	2015	1	N60107	Sequence encoding
c 603	14	1.0	1821	1	V71034	p38-green flouresc	c 677	14	1.0	2016	1	Q02887	CDNA of human plac
c 604	14	1.0	1821	1	V71025	p38-green flouresc	c 678	14	1.0	2019	1	Q85643	Poly-beta-hydroxya
c 605	14	1.0	1824	1	V71025	CDNA sequence enco	c 679	14	1.0	2028	1	Q48760	GAT-2 GABA transpo
c 606	14	1.0	1827	1	Q35685	HSA gene with fuse	c 680	14	1.0	2038	1	V33060	Oryza sativa RNA p
c 607	14	1.0	1827	1	T27599	Human serum albumi	c 681	14	1.0	2049	1	T16062	Murine ikaros CDNA
c 608	14	1.0	1827	1	V20403	HSA gene. Improved	c 682	14	1.0	2049	1	V66971	Mouse ikaros enco
c 609	14	1.0	1830	1	Q29765	HSA gene. Expressi	c 683	14	1.0	2049	1	V42808	Mouse ikaros isofo
c 610	14	1.0	1830	1	Q98695	Human serum albumi	c 684	14	1.0	2055	1	N30110	Sequence encoding
c 611	14	1.0	1830	1	T14580	Cancer metastasis	c 685	14	1.0	2055	1	X34159	Mycobacterium spec
c 612	14	1.0	1830	1	T27598	HSA gene with N-te	c 686	14	1.0	2057	1	T45098	Mycobacterium spec
c 613	14	1.0	1830	1	T27600	HSA gene with fuse	c 687	14	1.0	2061	1	X34160	Sequence of human
c 614	14	1.0	1830	1	T27601	HSA gene with C-te	c 688	14	1.0	2064	1	N92583	Human serum albumi
c 615	14	1.0	1830	1	T12924	Gene coding for HS	c 689	14	1.0	2064	1	T66701	Staphylococcus aur
c 616	14	1.0	1832	1	T12924	Gene coding for P6	c 690	14	1.0	2082	1	V74522	
c 617	14	1.0	1836	1	Q22196								

DNA encoding p34 f
DNA encoding p34 f
H. pylori inner me
H. pylori cell env
HCV CKS-ENV recomb
HCV CKS-ENV recomb
HCV CKS-ENV recomb
Mutant lipase codi
PHCV-104 - recomb
CDNA encoding chlm
Sequence of the pr
DNA encoding the m
Endotoxin Crya(c)
Carrot reverse tra
AAV4 Rep gene. Ade
AAV4 Rep 78 gene.
BUF-3 gene for hum
Arp 4 gene. New Sc
Sequence encoding
Human alpha lc adr
Jnk1-green floures
Jnk1-green floures
Jnk1-green floures
Encodes human Reti
Human retinoic aci
Genomic/CDNA compo
Sequence encoding
Mullerian inhibiti
Borrelia burgdorfe
Green fluorescent
Clone 19 encoding
DNA encoding malol
Fluorescent calmod
Fluorescent calmod
Heliothis ecodyson
DNA encoding a for
TCR delta protein
Fluorescent calmod
Human HFGAN72 rece
Human HFGAN72 rece
Fluorescent calmod
Truncated human al
H. pylori inner me
H. pylori ORF 06ep
cDNA coding for CM
Cytidine monophosp
Human truncated al
Human homeobox gen
Human alpha-1C adr
Human alpha-1C adr
Human melanoma ass
Human secreted pro
Human alpha-1C adr
H. pylori cell env
Human alpha-1C adr
DNA encoding TAP.
H. pylori cell env
Sequence encoding
CDNA of human plac
Poly-beta-hydroxya
GAT-2 GABA transpo
Oryza sativa RNA p
Murine ikaros CDNA
Mouse ikaros enco
Mouse ikaros isofo
Sequence encoding
Mycobacterium spec
Mycobacterium spec
Mycobacterium spec
Sequence of human
Human serum albumi
Staphylococcus aur

691	14	1.0	2085	1	Q81504	OPDE 45 kDa subuni	c 764	14	1.0	2462	1	X20299	Borrelia burgdorfe
692	14	1.0	2089	1	T31378	Human alpha-1C3 ad	765	14	1.0	2464	1	T45794	Heliothis eclysona
693	14	1.0	2093	1	Q70541	Hepatitis C virus	c 766	14	1.0	2472	1	T74953	Staphylococcus aur
694	14	1.0	2098	1	X02558	Human B1 cDNA, New	c 767	14	1.0	2503	1	T96475	MSRV-1 clone ITRGA
695	14	1.0	2127	1	T32346	Human adenylylcycl	c 768	14	1.0	2503	1	T43169	Clone ITRGAG12 DNA
696	14	1.0	2133	1	N91042	Promoter-enhancer	c 769	14	1.0	2506	1	T34184	Pentachlorophenol
697	14	1.0	2137	1	Q05675	v-PA-beta, New fib	c 770	14	1.0	2510	1	Q20690	hGrp-1 and huOG-1
698	14	1.0	2157	1	T71039	Erk2-green floures	771	14	1.0	2511	1	T71032	Grk5-green floures
699	14	1.0	2160	1	T71027	Smad2-green floures	c 772	14	1.0	2516	1	Q49737	Pcp B gene, Novel
700	14	1.0	2165	1	T14054	Fungal signal reco	773	14	1.0	2529	1	T71024	Grk5-green floures
701	14	1.0	2169	1	X23320	N. meningitidis st	774	14	1.0	2532	1	T71075	Green fluorescent
702	14	1.0	2175	1	Q56930	Bacillus thuringie	775	14	1.0	2537	1	N70917	Sequence encoding
703	14	1.0	2175	1	Q29268	Human calcium chan	776	14	1.0	2550	1	T47532	Cytomegalovirus To
704	14	1.0	2181	1	T71037	PXB-green flouresc	777	14	1.0	2550	1	T47534	Cytomegalovirus To
705	14	1.0	2184	1	T71086	Green fluorescent	778	14	1.0	2562	1	T71076	Protein tyrosine p
706	14	1.0	2192	1	T77838	Human melanoma ass	779	14	1.0	2575	1	T98572	DNA encoding a S.
707	14	1.0	2196	1	Q74211	CMVintA promoter a	780	14	1.0	2582	1	T90543	Maize male fertili
708	14	1.0	2196	1	T01112	CMVintA-GBH termin	c 781	14	1.0	2591	1	Q45961	HSA-vWF(470-713) f
709	14	1.0	2199	1	T80052	Rice actin 1 gene	782	14	1.0	2598	1	T71072	zap70-green floure
710	14	1.0	2206	1	Q70754	Beta tubulin gene	c 783	14	1.0	2603	1	T72148	DNA encoding trans
711	14	1.0	2224	1	Q70731	TARA-binding prote	784	14	1.0	2616	1	Q37966	Sequence encoding
712	14	1.0	2217	1	Q66982	Human betaine-GABA	785	14	1.0	2616	1	T71071	Green fluorescent
713	14	1.0	2217	1	T16542	Human betaine/GABA	786	14	1.0	2623	1	T51715	cDNA for adenoviru
714	14	1.0	2220	1	T11022	Urochloa panicolide	c 787	14	1.0	2629	1	N81338	Protein A gene wit
715	14	1.0	2247	1	V24920	H. pylori ORF 05ae	c 788	14	1.0	2629	1	Q24523	Vasopactive intesti
716	14	1.0	2247	1	V25134	H. pylori inner me	c 789	14	1.0	2631	1	T75434	Bacillus caldotena
717	14	1.0	2251	1	N30050	Sequence encoding	c 790	14	1.0	2631	1	T75432	DNA encoding Bacil
718	14	1.0	2251	1	X40195	Human albumin gene	c 791	14	1.0	2631	1	T75433	DNA encoding Bacil
719	14	1.0	2257	1	T015674	Neisseria meningit	792	14	1.0	2639	1	Q41259	2,2-dialkylglycine
720	14	1.0	2257	1	Q15270	v-PA-alpha2, New f	793	14	1.0	2639	1	Q72718	Dialkylglycine dec
721	14	1.0	2258	1	N60078	Recombinant human	c 794	14	1.0	2655	1	V32919	Solanum tuberosum
722	14	1.0	2262	1	X23322	N. meningitidis st	795	14	1.0	2659	1	Q51608	Moraxella bovis mb
723	14	1.0	2265	1	T14530	HSA:Fc gamma RII g	c 796	14	1.0	2662	1	V33136	Helicobacter leucy
724	14	1.0	2270	1	N91184	SprB gene encoding	c 797	14	1.0	2666	1	Q98236	Partial rice pyruv
725	14	1.0	2274	1	V90770	Nucleotide sequenc	798	14	1.0	2684	1	Q75136	Lactococcus lactis
726	14	1.0	2280	1	N60395	Sequence constitut	799	14	1.0	2692	1	Q51114	Sequence encoding
727	14	1.0	2280	1	Q89780	Human alpha 1c adr	c 800	14	1.0	2694	1	V62145	HSV-2 strain SB5 C
728	14	1.0	2292	1	V84357	Streptococcus pneu	801	14	1.0	2716	1	T42064	Human brain Na+ de
729	14	1.0	2307	1	V58945	B. breve essential	802	14	1.0	2716	1	V33503	Human sodium-lithi
730	14	1.0	2306	1	T31377	Human alpha-1C2 ad	803	14	1.0	2724	1	Q78166	Human cytomagalovi
731	14	1.0	2315	1	V07281	Human semaphorin W	804	14	1.0	2724	1	T47527	Human cytomagalovi
732	14	1.0	2330	1	Q20759	Alkaline protease	805	14	1.0	2724	1	T91280	Human cytomagalovi
733	14	1.0	2337	1	T94212	Thermotoga maritim	806	14	1.0	2741	1	V36300	Murine guanine nuc
734	14	1.0	2338	1	Q13575	DHR3 gene, DNA enc	c 807	14	1.0	2745	1	Q92655	Virulence determin
735	14	1.0	2341	1	V62155	HSV-2 strain SB5 C	c 808	14	1.0	2745	1	Q92657	Virulence determin
736	14	1.0	2343	1	V36302	Murine guanine nuc	809	14	1.0	2745	1	T45795	Heliothis eclysona
737	14	1.0	2360	1	Q02888	Human placenta-der	c 810	14	1.0	2745	1	V38109	Mycobacterium bovi
738	14	1.0	2360	1	Q24438	EGF/HB-EHM, Hepari	c 811	14	1.0	2745	1	V38108	Mycobacterium bovi
739	14	1.0	2364	1	Q12632	CD4-specific CDR-g	c 812	14	1.0	2746	1	T72893	Rabbit protein-cou
740	14	1.0	2373	1	Q45455	Sequence encoding	c 813	14	1.0	2751	1	X30434	H. pylori cellular
741	14	1.0	2379	1	Q10548	Prepro-HSA-VIV2 fu	c 814	14	1.0	2760	1	X25097	Bacillus subtilis
742	14	1.0	2382	1	Q45987	Prepro-HSA-G-CSF c	c 815	14	1.0	2768	1	Q10502	Polyhydroxybutyrat
743	14	1.0	2384	1	Q46543	Drosophila SSRP c	c 816	14	1.0	2770	1	T78599	AS-30D tumour Type
744	14	1.0	2384	1	V09624	D. melanogaster SS	c 817	14	1.0	2778	1	V25138	H. pylori cell env
745	14	1.0	2387	1	Q48438	Brh-1 cDNA, Polype	c 818	14	1.0	2784	1	T68270	H. pylori cytoplas
746	14	1.0	2387	1	T45675	Wasp Brh-1 toxin g	819	14	1.0	2799	1	V71085	PKG-green fluoresc
747	14	1.0	2394	1	V71088	NFKappaB p65 subun	c 820	14	1.0	2802	1	V71084	Green fluorescent
748	14	1.0	2394	1	V71087	PKB-green fluoresc	c 821	14	1.0	2833	1	Q32648	S receptor kinase
749	14	1.0	2395	1	V90864	Nucleotide sequenc	822	14	1.0	2833	1	V36301	Murine guanine nuc
750	14	1.0	2418	1	V71040	Smad4-green floure	823	14	1.0	2845	1	T93093	Human GCF1 cDNA, P
751	14	1.0	2418	1	T15598	Laccase-LCC1 gene.	824	14	1.0	2854	1	V32591	Schwannomin-bindin
752	14	1.0	2421	1	V71028	Green fluorescent	c 825	14	1.0	2871	1	Q14807	B.thuringiensis to
753	14	1.0	2427	1	V07515	Helicobacter pylori	c 826	14	1.0	2898	1	T68848	Photocorhabdus lumin
754	14	1.0	2430	1	Q04305	Coding region of m	827	14	1.0	2899	1	Q86757	Construct comprisi
755	14	1.0	2430	1	T61550	Murine interleukin	828	14	1.0	2899	1	T14053	Fungal signal reco
756	14	1.0	2430	1	V17655	Mouse interleukin-	829	14	1.0	2907	1	V71026	p85alpha-green flo
757	14	1.0	2430	1	V38332	Mouse interleukin-	c 830	14	1.0	2911	1	V00133	Hexokinase-glucoki
758	14	1.0	2430	1	V08858	Mouse interleukin-	c 831	14	1.0	2911	1	V00099	Hexokinase-glucoki
759	14	1.0	2430	1	X22407	Murine IL-4 recept	c 832	14	1.0	2911	1	V00124	Hexokinase-glucoki
760	14	1.0	2433	1	T29396	Apoptosis particip	c 833	14	1.0	2911	1	V00098	Hexokinase-glucoki
761	14	1.0	2438	1	T38687	Mus musculus SOCS1	834	14	1.0	2911	1	V05709	Human Th2/B19 cDNA
762	14	1.0	2454	1	T32864	Tomato P119 gene p	835	14	1.0	2913	1	V71035	p85alpha-green flo
763	14	1.0	2455	1	Q45988	G-CSF-(Gly)4-HSA C	836	14	1.0	2917	1	Q86758	Construct comprisi

c 837	14	1.0	2955	1	V20404	Plasmid R-H-R/SK #	c 910	14	1.0	3603	1	T79595	TATA-binding prote
c 838	14	1.0	2959	1	O86756	Construct compri	c 911	14	1.0	3610	1	V00669	Synthetic hepatiti
c 839	14	1.0	2962	1	X21408	targetting region	c 912	14	1.0	3635	1	V00125	Rat hexokinase II
c 840	14	1.0	2965	1	X39658	Renal cancer assoc	c 913	14	1.0	3635	1	V00086	Rat hexokinase II
c 841	14	1.0	2971	1	N81166	fdHF gene New reco	c 914	14	1.0	3647	1	V00159	Rat hexokinase I e
c 842	14	1.0	2991	1	V71078	IkappaB kinase alp	c 915	14	1.0	3647	1	V00085	Rat hexokinase I e
c 843	14	1.0	2991	1	X20288	Borrelia burgdorfe	c 916	14	1.0	3704	1	T59938	Phage resistance g
c 844	14	1.0	2991	1	V29925	tcca gene from the	c 917	14	1.0	3733	1	V74849	Staphylococcus aur
c 845	14	1.0	2994	1	V71077	Green fluorescent	c 918	14	1.0	3733	1	V74849	Staphylococcus aur
c 846	14	1.0	3000	1	Q14319	Pertactin antigen	c 919	14	1.0	3748	1	Q23006	Actin gene (incli
c 847	14	1.0	3000	1	Q14320	Pertactin antigen	c 920	14	1.0	3748	1	Q48535	Actin. Novel polyp
c 848	14	1.0	3000	1	Q26509	Bordetella parap	c 921	14	1.0	3748	1	Q48535	Sf9 alpha-mannosid
c 849	14	1.0	3000	1	Q34566	prn gene. DNA enco	c 922	14	1.0	3748	1	V16776	Sf9 alpha-mannosid
c 850	14	1.0	3012	1	V52012	Helicobacter poly	c 923	14	1.0	3750	1	Q22203	A. chrysogenum act
c 851	14	1.0	3029	1	X20286	Borrelia burgdorfe	c 924	14	1.0	3756	1	T72684	Sugar biosynthesis
c 852	14	1.0	3032	1	V20992	Alcaligenes specie	c 925	14	1.0	3771	1	Q20336	B.thuringiensis to
c 853	14	1.0	3101	1	X14217	H. pylori GHPO 111	c 926	14	1.0	3771	1	Q30805	Toxin gene 33f2. N
c 854	14	1.0	3106	1	T99905	Enterohaemorrhagic	c 927	14	1.0	3771	1	Q31411	Bacillus thuringie
c 855	14	1.0	3106	1	V02323	Enterohaemorrhagic	c 928	14	1.0	3771	1	Q32161	BT toxin 33f2 Nema
c 856	14	1.0	3107	1	V68092	CDNA encoding the	c 929	14	1.0	3771	1	Q30937	BT toxin 33f2. New
c 857	14	1.0	3110	1	T84234	DNA encoding an au	c 930	14	1.0	3771	1	Q51689	Bacillus thuringie
c 858	14	1.0	3110	1	V53557	DNA encoding 2 sta	c 931	14	1.0	3771	1	Q94055	Strain 33f2 DNA. D
c 859	14	1.0	3120	1	V71029	Green fluorescent	c 932	14	1.0	3771	1	T60071	33f2 toxin coding
c 860	14	1.0	3125	1	Q73686	HIV virus-1(LAI) g	c 933	14	1.0	3796	1	T93499	Xenopus frog prote
c 861	14	1.0	3131	1	O66687	EHEC eae gene asso	c 934	14	1.0	3822	1	T84151	DNA encoding a mer
c 862	14	1.0	3131	1	T99904	Enterohaemorrhagic	c 935	14	1.0	3822	1	T84151	Phospholipase C-ga
c 863	14	1.0	3131	1	V02322	Enterohaemorrhagic	c 936	14	1.0	3877	1	T12292	CDNA of leaderless
c 864	14	1.0	3131	1	V40561	Human thiazide-sen	c 937	14	1.0	3893	1	T12293	Phospholipase C-ga
c 865	14	1.0	3138	1	V71041	Stat5-green floure	c 938	14	1.0	3895	1	V52334	Streptococcus pneu
c 866	14	1.0	3141	1	T47556	Human cytomegalovi	c 939	14	1.0	3896	1	X05816	Mouse pheromone re
c 867	14	1.0	3183	1	V09024	Homo sapiens 20q13	c 940	14	1.0	3919	1	X10355	Human tolloid-like
c 868	14	1.0	3240	1	V48270	A. chrysogenum gam	c 941	14	1.0	3932	1	Q64112	cryET5 gene. Isola
c 869	14	1.0	3246	1	Q54170	B.stearothermophil	c 942	14	1.0	3934	1	T84834	CryET5 gene. Bacil
c 870	14	1.0	3252	1	Q31650	Bacillus caldorena	c 943	14	1.0	3934	1	T95051	DNA encoding Bacil
c 871	14	1.0	3303	1	Q14806	B.thuringiensis to	c 944	14	1.0	3955	1	V83927	DNA encoding a Cry
c 872	14	1.0	3311	1	T70377	Cytohesin 1. Cyto	c 945	14	1.0	3955	1	V15181	Human serrate 2 en
c 873	14	1.0	3317	1	T97089	Bacillus stearothe	c 946	14	1.0	4029	1	X13235	Nucleotide sequenc
c 874	14	1.0	3339	1	V61096	Mouse membrane typ	c 947	14	1.0	4075	1	T47557	Enterococcus faeca
c 875	14	1.0	3350	1	T08553	Oncogene R-ras mut	c 948	14	1.0	4166	1	N90528	42K promoted cytom
c 876	14	1.0	3358	1	V58005	Rat neuturin rece	c 949	14	1.0	4200	1	Q48652	DNA sequence encod
c 877	14	1.0	3377	1	V64424	Mouse elf cDNA. Ne	c 950	14	1.0	4200	1	Q45166	43 kDa/156 kDa non
c 878	14	1.0	3412	1	X25772	S.erythraea erythr	c 951	14	1.0	4200	1	Q98503	Sequence of precur
c 879	14	1.0	3420	1	T75437	Mortierella alpina	c 952	14	1.0	4200	1	T97316	Rabbit 97 kDa dyst
c 880	14	1.0	3423	1	X40183	Lung cancer associ	c 953	14	1.0	4200	1	T97316	Rabbit (156 kDa) d
c 881	14	1.0	3435	1	Q79746	Mycoplasma pirum a	c 954	14	1.0	4239	1	V74644	Staphylococcus aur
c 882	14	1.0	3445	1	Q48230	Acromonium chrysog	c 955	14	1.0	4239	1	X13387	Enterococcus faeca
c 883	14	1.0	3445	1	Q55405	A.chrysogenum beta	c 956	14	1.0	4260	1	T47528	H6 promoted cyto
c 884	14	1.0	3445	1	Q55406	A.chrysogenum beta	c 957	14	1.0	4268	1	T00052	Hepatitis GB virus
c 885	14	1.0	3451	1	V02308	Cell membrane prot	c 958	14	1.0	4278	1	V52286	Streptococcus pneu
c 886	14	1.0	3456	1	T85397	Pseudomonas flure	c 959	14	1.0	4299	1	V03310	Pyrololobus fumari
c 887	14	1.0	3463	1	Q27180	Alkaline cellulase	c 960	14	1.0	4300	1	Q25812	Clone 45-A. Mammal
c 888	14	1.0	3471	1	V16516	DNA encoding a Bac	c 961	14	1.0	4315	1	V63754	Human JAGGED2 cDNA
c 889	14	1.0	3474	1	Q39018	Sequence of pure m	c 962	14	1.0	4328	1	V21684	Vector plasmid CMV
c 890	14	1.0	3474	1	Q39018	Sequence of pure m	c 963	14	1.0	4328	1	X24808	Vector CMVkm2. Lip
c 891	14	1.0	3474	1	T74012	Maize optimised-B.	c 964	14	1.0	4330	1	V26524	Plasmid pTLP2 enco
c 892	14	1.0	3474	1	T74012	Maize optimised-B.	c 965	14	1.0	4344	1	Q56782	Insecticidal toxin
c 893	14	1.0	3474	1	V16191	Maize optimised DN	c 966	14	1.0	4373	1	T72119	Nucleotide sequenc
c 894	14	1.0	3478	1	V16191	Maize optimised DN	c 967	14	1.0	4395	1	V65398	Pyruvate:flavodoxi
c 895	14	1.0	3478	1	V00291	Insecticidal prote	c 968	14	1.0	4432	1	Q74206	DNA encoding an an
c 896	14	1.0	3484	1	V00395	Insecticidal gene	c 969	14	1.0	4432	1	T01113	Expression vector
c 897	14	1.0	3505	1	Q35270	Human GTA cDNA. De	c 970	14	1.0	4453	1	T69890	Human cyclin D1-hu
c 898	14	1.0	3508	1	Q39020	Sequence of full l	c 971	14	1.0	4453	1	V54118	Human cyclin D1/cy
c 899	14	1.0	3508	1	T74013	Full length maize	c 972	14	1.0	4483	1	T40091	Human Serrate-2 (H
c 900	14	1.0	3508	1	V16192	Maize optimised DN	c 973	14	1.0	4540	1	T69891	Human cyclin D1-hu
c 901	14	1.0	3516	1	V71082	Green fluorescent	c 974	14	1.0	4540	1	V54119	Human cyclin D1/cy
c 902	14	1.0	3546	1	V71083	NFAT1-green floure	c 975	14	1.0	4575	1	N91465	Drosophila melanog
c 903	14	1.0	3547	1	T01115	Expression vector	c 976	14	1.0	4588	1	V02185	Murine type C lect
c 904	14	1.0	3547	1	V21771	VIR vaccination ve	c 977	14	1.0	4590	1	N60472	Sequence encoding
c 905	14	1.0	3553	1	Q74208	Expression vector	c 978	14	1.0	4594	1	T47533	CMV gB transmembr
c 906	14	1.0	3557	1	X04605	Maize genomic clon	c 979	14	1.0	4594	1	T47533	CMV gB transmembr
c 907	14	1.0	3567	1	T47559	42K promoted cytom	c 980	14	1.0	4621	1	T69889	Human cyclin D1-hu
c 908	14	1.0	3569	1	T85905	Polygalacturonase	c 981	14	1.0	4621	1	V54117	Human cyclin D1/cy
c 909	14	1.0	3603	1	T42217	Human TATA-binding	c 982	14	1.0	4700	1	V30461	Soybean seed coat

C 983 14 1.0 4767 1 V21648 AAV4 genome. Adeno
 C 984 14 1.0 4768 1 T47531 H6 promoted cytochrome
 C 985 14 1.0 4771 1 V02186 Human type C lectin
 C 986 14 1.0 4809 1 Q62185 PAQ1 plasmid fragm
 C 987 14 1.0 4818 1 V21686 Vector plasmid CMV
 C 988 14 1.0 4832 1 V74500 Staphylococcus aur
 C 989 14 1.0 4839 1 Q06827 Alpha amylase pull
 C 990 14 1.0 4864 1 Q74207 Expression vector
 C 991 14 1.0 4864 1 T01114 Expression vector
 C 992 14 1.0 4864 1 V21737 VIJneo sequence us
 C 993 14 1.0 4881 1 V63438 feline herpesvirus
 C 994 14 1.0 4909 1 T47558 42K promoted cytom
 C 995 14 1.0 4912 1 X08423 Recombinant vector
 C 996 14 1.0 4919 1 Q29280 Human calcium chan
 C 997 14 1.0 4928 1 T32656 Plasmid encoding h
 C 998 14 1.0 4942 1 X00461 Human type VI aden
 C 999 14 1.0 4956 1 X13228 Enterococcus faeca
 C1000 14 1.0 4973 1 V58289 S. pyogenes SP-55-

ALIGNMENTS

RESULT 1
 X13598
 ID X13598 standard; DNA; 965 BP.
 AC X13598;
 AT 19-MAR-1999 (first entry)
 DE Enterococcus faecalis genome contig SEQ ID NO:661.
 KW Enterococcus faecalis; contig; detection; Enterococcal infection;
 OS vaccine; attenuation; computer readable medium; ds.
 PS Enterococcus faecalis.
 PN WO9850555-A2.
 PD 12-NOV-1998.
 PF 04-MAY-1998; U08985.
 PR 14-NOV-1997; US-066009.
 PR 06-MAY-1997; US-044031.
 PR 16-MAY-1997; US-046655.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Barash SC, Dillon PJ, Kunsch CA;
 DR WPI; 99-045171/04.
 PT New Isolated Enterococcus faecalis polynucleotides and polypeptides
 PT - used to develop products for the detection of Enterococcus and for
 PT use in vaccines for prevention or attenuation of Enterococcus
 PT infection.
 PS Claim 1; Page 1907; 2084pp; English.
 CC A computer readable medium has been developed which has recorded on it
 CC 982 nucleotide sequences isolated from the Enterococcus faecalis genome.
 CC X12938 to X13919 represent these nucleotide sequences which are primary
 CC nucleotide sequences, also known as contigs. The computer-based system
 CC can identify fragments of the Enterococcus faecalis genome with
 CC commercial importance. The products can be used to detect the presence
 CC of Enterococcus faecalis in samples. They can also be used for
 CC diagnosing Enterococcal infection in an animal and monitoring
 CC progression of disease, and for identifying agents which can be used to
 CC modulate the growth or pathogenicity of Enterococcus faecalis, or
 CC another related organism, in vivo or in vitro. In particular the
 CC polypeptides encoded by the Enterococcus faecalis nucleotide sequences
 CC can be used in vaccines to prevent or attenuate an Enterococcal
 CC infection.
 SQ Sequence 965 BP; 288 A; 173 C; 133 G; 367 T;

Query Match 1.3%; Score 18; DB 1; Length 965;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 caaaaaagaagcatcctt 110
 Db 197 CAAAAAAGAGCATCCTT 214
 ||||||||||||||||

RESULT 2

V58939
 ID V58939 standard; DNA; 9960 BP.
 AC V58939;
 AT 15-FEB-1999 (first entry)
 DE Mycobacterium smegmatis embCAB operon.
 KW Drug resistance; antibiotic resistance; antimycobacterial;
 KW ethambutol; embCAB operon; infection; vaccine; therapy; ds.
 OS Mycobacterium smegmatis.
 PN WO9841533-A1.
 PD 24-SEP-1998.
 PF 16-MAR-1998; U05128.
 PR 20-MAR-1997; US-822586.
 PA (YESH) UNIV YESHIVA EINSTEIN COLLEGE.
 PI Jacobs WR, Musser J, Telenti A;
 DR WPI; 98-521160/44.
 DR P-PSDB; W73055-57.
 PT Wild type and mutated sequences of Mycobacterium embCAB operon -
 PT useful to e.g. identify ethambutol-resistant mycobacterial strains
 PT and produce antisense sequences to treat mycobacterial infections
 PS Disclosure; Fig 6A-I; 62pp; English.
 CC This is the DNA sequence of the Mycobacterium smegmatis embCAB
 CC operon, which determines resistance to the antimycobacterial drug
 CC ethambutol (EMB). It includes the embA, embC and embB genes that
 CC encode proteins (see W73052-54) which are the target of action of
 CC M. smegmatis for EMB. To identify genes conferring EMB resistance,
 CC a genomic library from a high level EMB-resistant mutant of M.
 CC smegmatis was introduced into wild-type M. smegmatis mc2155. Four
 CC overlapping cosmids were identified which conferred a resistant
 CC phenotype. The minimum size fragment capable of conferring EMB
 CC resistance was 9 kb (pIMW99). pIMW99 plus 7 kb upstream M.
 CC smegmatis sequence was determined revealing 3 homologous open
 CC reading frames (embC, embB, embB) and 4 additional potential coding
 CC regions. Wild-type and mutated embCAB nucleic acid sequences are
 CC useful as probes used in the diagnosis of drug-resistant
 CC mycobacteria or to determine the susceptibility of mycobacteria to
 CC EMB. The nucleic acids are also useful in the treatment of
 CC mycobacterial infections; anti-DNA or anti-RNA sequences can be
 CC administered to inhibit embCAB operon mRNA activity (claimed). The
 CC invention additionally provides for the use of embCAB operon
 CC nucleic acid sequences as vaccines, or to improve existing
 CC vaccines.
 SQ Sequence 9960 BP; 1389 A; 3592 C; 3360 G; 1618 T;

Query Match 1.3%; Score 18; DB 1; Length 9960;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 401 acgggtacatctctgacca 418
 Db 956 ACGGCTACATCTCTGACCA 973
 ||||||||||||||||

RESULT 3

V58938
 ID V58938 standard; DNA; 10095 BP.
 AC V58938;
 AT 15-FEB-1999 (first entry)
 DE Mycobacterium tuberculosis embCAB operon.
 KW Drug resistance; antibiotic resistance; antimycobacterial;
 KW ethambutol; embCAB operon; infection; vaccine; therapy;
 KW tuberculosis; ds.
 OS Mycobacterium tuberculosis.
 PN WO9841533-A1.
 PD 24-SEP-1998.
 PF 16-MAR-1998; U05128.
 PR 20-MAR-1997; US-822586.
 PA (YESH) UNIV YESHIVA EINSTEIN COLLEGE.
 PI Jacobs WR, Musser J, Telenti A;
 DR WPI; 98-521160/44.
 DR P-PSDB; W73052-54.
 PT Wild type and mutated sequences of Mycobacterium embCAB operon -
 PT useful to e.g. identify ethambutol-resistant mycobacterial strains

PT and produce antisense sequences to treat mycobacterial infections
PS Disclosure; Fig 4A-I: 62pp; English.

CC This is the DNA sequence of the Mycobacterium tuberculosis embCAB
CC operon, which determines resistance to the antimycobacterial drug
CC ethambutol (EMB). It includes the embA, embC and embB genes
CC that encode proteins (see W73052-54) which are the target of
CC action of M. tuberculosis for EMB. Wild-type and mutated embCAB
CC nucleic acid sequences are useful e.g. as probes used in the
CC diagnosis of drug-resistant mycobacteria or to determine the
CC susceptibility of mycobacteria to EMB. The nucleic acids are also
CC useful in the treatment of mycobacterial infections; anti-DNA or
CC anti-RNA sequences can be administered to inhibit embCAB operon
CC mRNA activity (claimed). The invention additionally provides for
CC the use of embCAB operon nucleic acid sequences as vaccines, or
CC to improve existing vaccines.

SQ Sequence 10095 BP; 1469 A; 3475 C; 3370 G; 1780 T;

Query Match 1.3%; Score 18; DB 1; Length 10095;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 401 acggctacatcctgacca 418

|||||

DB 1031 ACGGTACATCCTGACCA 1048

RESULT 4

T19263

ID T19263 standard; cDNA to mRNA; 196 BP.

AC T19263;

DE 28-JUN-1996 (first entry)

DE Human gene signature HUMGS00280.

KW Gene signature; messenger RNA; mRNA; relative abundance; frequency;

KW human; cloning; mapping; non-biased library; diagnosis; detection;

KW cell typing; abnormal cell function; ss.

OS Homo sapiens.

PN WO9514772-A1.

PD 01-JUN-1995.

PF 11-NOV-1994; J01916.

PR 12-NOV-1993; JP-355504.

PA (MATSU) MATSUBARA K.

PA (OKUBU) OKUBO K.

PI Matsubara K, Okubo K;

PI WPI: 95-206931/27.

DR Identifying gene signatures in 3'-directed human cDNA library - e.g.

PT for diagnosis of abnormal cell function, by preparing cDNA that

PT reflects relative abundance of corresp. mRNA in specific human

PT tissues

PS Claim 1; Page 345; 2245pp; Japanese.

CC A single-stranded DNA (or its complementary strand or the corresp.

CC double-stranded DNA) which comprises one of the 7837 "GS" sequences

CC given in T19001-T26837 and which is able to hybridise to part of

CC human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)

CC sequences were obtained from 3'-directed cDNA libraries prepared

CC from various human tissues; synthesis of cDNA was initiated from the

CC 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-

CC untranslated sequence is unique to a particular mRNA species, almost

CC all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library

CC is constructed so as to reflect accurately the relative abundance of

CC different mRNAs in the particular tissue from which it was derived.

CC The appearance frequency of a given GS in a cDNA library can be

CC determined (esp. using primers and probes derived from the GS

CC sequences) as a means of diagnosing abnormal cell function or for

CC recognising different cell types.

SQ Sequence 196 BP; 59 A; 55 C; 34 G; 48 T;

Query Match

Best Local Similarity 1.2%; Score 17; DB 1; Length 196;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 709 accgacgttgccatcaa 725

DB 64 ACGACGTTGCCATCAA 80

|||||

RESULT 5

V31989/C

ID V31989 standard; DNA; 229 BP.

AC V31989;

DE 25-SEP-1998 (first entry)

DE BS106 polynucleotide clone 1662885 (1).

KW ss; human; BS106; breast tissue gene; breast cancer; detection marker.

OS Homo sapiens.

PN WO9818945-A1.

PD 07-MAY-1998.

PF 31-OCT-1997; U19836.

PR 31-OCT-1996; US-742067.

PA (ABBO) ABBOTT LAB.

PI Gordon J, Granados EN, Hodges SC, Klass MR, Kratochvil JD,

PI Roberts-Rapp L, Russell JC, Stroupe SD;

PI WPI: 98-272234/24.

DR Detecting BS106 gene products - useful for developing products for

PT detecting, staging, preventing, treating or determining

PT predisposition to e.g. breast cancer

PS Claim 1; Page 88; 114pp; English.

CC BS106 is a breast tissue gene with which breast cancer and related

CC diseases are associated. The BS106 polynucleotides V31989-V31993 can be

CC detected by BS106 specific polynucleotides or complements acting as

CC useful markers for detection methods. The products and methods can be

CC used for detecting, diagnosing, staging, preventing or treating, or

CC determining predisposition to diseases or conditions of the breast such

CC as breast cancer.

SQ Sequence 229 BP; 43 A; 58 C; 50 G; 62 T;

Query Match

Best Local Similarity 1.2%; Score 17; DB 1; Length 229;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 381 gggcttcacatcagca 397

|||||

DB 187 GGGCTTCATCATGCA 171

RESULT 6

V31990/C

ID V31990 standard; DNA; 308 BP.

AC V31990;

DE 25-SEP-1998 (first entry)

DE BS106 polynucleotide clone 893988.

KW ss; human; BS106; breast tissue gene; breast cancer; detection marker.

OS Homo sapiens.

PN WO9818945-A1.

PD 07-MAY-1998.

PF 31-OCT-1997; U19836.

PR 31-OCT-1996; US-742067.

PA (ABBO) ABBOTT LAB.

PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN,

PI Gordon J, Granados EN, Hodges SC, Klass MR, Kratochvil JD,

PI Roberts-Rapp L, Russell JC, Stroupe SD;

PI WPI: 98-272234/24.

DR Detecting BS106 gene products - useful for developing products for

PT detecting, staging, preventing, treating or determining

PT predisposition to e.g. breast cancer

PS Claim 1; Page 89; 114pp; English.

CC BS106 is a breast tissue gene with which breast cancer and related

CC diseases are associated. The BS106 polynucleotides V31989-V31993 can be

CC detected by BS106 specific polynucleotides or complements acting as

CC useful markers for detection methods. The products and methods can be

CC used for detecting, diagnosing, staging, preventing or treating, or

CC determining predisposition to diseases or conditions of the breast such

CC as breast cancer.

SQ Sequence 308 BP; 63 A; 94 C; 65 G; 86 T;

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Query Match          1.2%; Score 17; DB 1; Length 308;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 381 gggttcattcatcagca 397
DB 174 GGGCTTCATCATCAGCA 158

RESULT 7
V31992/c
ID V31992 standard; DNA; 482 BP.
AC V31992.
DT 25-SEP-1998 (first entry)
DE BS106 polynucleotide consensus sequence.
KW ss: human; BS106; breast tissue gene; breast cancer; detection marker.
OS Homo sapiens.
PN WO9818945-A1.
PD 07-MAY-1998.
PF 31-OCT-1997; U19836.
PR 31-OCT-1996; US-742067.
PA (ABRO ) ABBOTT LAB.
PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN.
PI Gordon J, Granados EN, Hodges SC, Klass MR, Kratochvil JD,
PI Roberts-Rapp L, Russell JC, Stroupe SD;
DR WPI; 98-272234/24.
PT Detecting BS106 gene products - useful for developing products for
PT detecting, staging, preventing, treating or determining
PT predisposition to e.g. breast cancer
PS Claim 1; Page 88; 114pp; English.
CC BS106 is a breast tissue gene with which breast cancer and related
CC diseases are associated. The BS106 polynucleotides V31989-V31993 can be
CC detected by BS106 specific polynucleotides or complements acting as
CC useful markers for detection methods. The products and methods can be
CC used for detecting, diagnosing, staging, preventing or treating, or
CC determining predisposition to diseases or conditions of the breast such
CC as breast cancer.
SQ Sequence 482 BP; 109 A; 136 C; 90 G; 145 T;

Query Match          1.2%; Score 17; DB 1; Length 482;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 381 gggttcattcatcagca 397
DB 187 GGGCTTCATCATCAGCA 171

RESULT 8
X00704/c
ID X00704 standard; DNA; 489 BP.
AC X00704;
DT 25-MAR-1999 (first entry)
DE Human secreted protein gene 34 clone HMQAJ64.
DE Human secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
OS Homo sapiens.
PN WO9842738-A1.
PD 01-OCT-1998.
PF 19-MAR-1998; U05311.
PR 30-MAR-1997; US-050937.
PR 21-MAR-1997; US-041276.
PR 21-MAR-1997; US-041277.
PR 21-MAR-1997; US-041281.

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PR 21-MAR-1997; US-042344.
PR 30-MAY-1997; US-048069.
PR 30-MAY-1997; US-048094.
PR 30-MAY-1997; US-048095.
PR 30-MAY-1997; US-048096.
PR 30-MAY-1997; US-048099.
PR 30-MAY-1997; US-048131.
PR 30-MAY-1997; US-048135.
PR 30-MAY-1997; US-048154.
PR 30-MAY-1997; US-048160.
PR 30-MAY-1997; US-048186.
PR 30-MAY-1997; US-048187.
PR 30-MAY-1997; US-048188.
PR 30-MAY-1997; US-048350.
PR 30-MAY-1997; US-048351.
PR 30-MAY-1997; US-048352.
PR 30-MAY-1997; US-048355.
PR 05-AUG-1997; US-054804.
PA (HUMA-) HUMAN GENOME SCI INC.
PI Brewer LA, Duan R, Ebner R, Ferrie AM, Florence KA,
PI Greene JM, Hu JS, Lafleur DW, Moore PA, NI J, Olsen HS,
PI Rosen CA, Ruben SM, Shi Y, Young P;
DR WPI; 99-070066/06.
DR P-PSDB; W67900.
PT New isolated human genes and the secreted polypeptides they encode -
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders
PS Claim 1; Page 234; 385pp; English.
CC This sequence represents a nucleic acid molecule which encodes a secreted
CC human protein. The gene number, and the clone it is derived from, are
CC detailed in the descriptor line. The gene can be used to generate fusion
CC proteins by linking to the gene to a human immunoglobulin Fc portion
CC (e.g. X00602) for increasing the stability of the fused protein as
CC compared to the human protein only.
CC The invention relates to 87 novel genes and their fragments (nucleic acid
CC sequences: X00611-X00724; amino acid sequences W67807-W68004) which
CC are useful for preventing, treating or ameliorating medical conditions
CC e.g. by protein or gene therapy. Also, pathological conditions can be
CC diagnosed by determining the amount of the new polypeptides in a sample
CC or by determining the presence of mutations in the new polynucleotides.
CC Specific uses are described for each of the 87 polynucleotides, based on
CC which tissues they are most highly expressed in (see X00611 for described
CC uses).
SQ Sequence 489 BP; 124 A; 134 C; 91 G; 140 T;

Query Match          1.2%; Score 17; DB 1; Length 489;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 381 gggttcattcatcagca 397
DB 181 GGGCTTCATCATCAGCA 165

RESULT 9
X00644/c
ID X00644 standard; DNA; 489 BP.
AC X00644;
DT 25-MAR-1999 (first entry)
DE Human secreted protein gene 34 clone HMQAJ64.
DE Human secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
OS Homo sapiens.
PN WO9842738-A1.
PD 01-OCT-1998.
PF 19-MAR-1998; U05311.

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PR 30-MAY-1997; US-050937.
PR 21-MAR-1997; US-041276.
PR 21-MAR-1997; US-041277.
PR 21-MAR-1997; US-041281.
PR 21-MAR-1997; US-042344.
PR 30-MAY-1997; US-048069.
PR 30-MAY-1997; US-048094.
PR 30-MAY-1997; US-048095.
PR 30-MAY-1997; US-048096.
PR 30-MAY-1997; US-048099.
PR 30-MAY-1997; US-048131.
PR 30-MAY-1997; US-048135.
PR 30-MAY-1997; US-048154.
PR 30-MAY-1997; US-048160.
PR 30-MAY-1997; US-048186.
PR 30-MAY-1997; US-048187.
PR 30-MAY-1997; US-048188.
PR 30-MAY-1997; US-048350.
PR 30-MAY-1997; US-048351.
PR 30-MAY-1997; US-048352.
PR 30-MAY-1997; US-048355.
PR 05-AUG-1997; US-054804.
PR (HUMA-) HUMAN GENOME SCI INC.
PI Brewer LA, Duan R, Ebner R, Ferrie AM, Florence KA,
PI Greene JM, Hu JS, Lafleur DW, Moore PA, Ni J, Olsen HS,
PI Rosen CA, Ruben SM, Shi Y, Young P;
DR WPI: 99-070066/06.
DR P-PSDB: W67840.
PT New isolated human genes and the secreted polypeptides they encode -
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders
PS Claim 1; Page 198; 385pp; English.
CC This sequence represents a nucleic acid molecule which encodes a secreted
CC human protein. The gene number, and the clone it is derived from, are
CC detailed in the descriptor line. The gene can be used to generate fusion
CC proteins by linking to the gene to a human immunoglobulin Fc portion
CC (e.g. X00602) for increasing the stability of the fused protein as
CC compared to the human protein only.
CC The invention relates to 87 novel genes and their fragments (nucleic acid
CC sequences: X00611-X00724; amino acid sequences W67807-W68004) which
CC are useful for preventing, treating or ameliorating medical conditions
CC e.g. by protein or gene therapy. Also, pathological conditions can be
CC diagnosed by determining the amount of the new polypeptides in a sample
CC or by determining the presence of mutations in the new polynucleotides.
CC Specific uses are described for each of the 87 polynucleotides, based on
CC which tissues they are most highly expressed in (see X00611 for described
CC uses).
SQ Sequence 489 BP; 125 A; 134 C; 87 G; 143 T;

Query Match 1.2%; Score 17; DB 1; Length 489;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 381 gggcttcacatcagca 397
DB 178 GGGCTTCATCATCAGCA 162

RESULT 10
V31993/C
ID V31993 standard; DNA; 553 BP.
AC V31993;
DE 25-SEP-1998 (first entry)
DE BS106 polynucleotide clone 1662885 (ii).
KW ss: human; BS106; breast tissue gene; breast cancer; detection marker.
OS Homo sapiens.
PN WO9818945-A1.
PD 07-MAY-1998.
PF 31-OCT-1997; U19836.
PF 31-OCT-1996; US-742067.
PA (ABBO ) ABBOTT LAB.
PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN,
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PI Gordon J, Granados EN, Hodges SC, Klass MR, Kratochvil JD,
PI Roberts-Rapp L, Russell JC, Stroupe SD;
DR WPI: 98-272234/24.
PT Detecting BS106 gene products - useful for developing products for
PT detecting, staging, preventing, treating or determining
PT predisposition to e.g. breast cancer
PS Claim 1; Page 90; 114pp; English.
CC BS106 is a breast tissue gene with which breast cancer and related
CC diseases are associated. The BS106 polynucleotides V31989-V31993 can be
CC detected by BS106 specific polynucleotides or complements acting as
CC useful markers for detection methods. The products and methods can be
CC used for detecting, diagnosing, staging, preventing or treating, or
CC determining predisposition to diseases or conditions of the breast such
CC as breast cancer.
SQ Sequence 553 BP; 159 A; 144 C; 101 G; 148 T;

Query Match 1.2%; Score 17; DB 1; Length 553;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 381 gggcttcacatcagca 397
DB 201 GGGCTTCATCATCAGCA 185

RESULT 11
V29521
ID V29521 standard; cDNA; 732 BP.
AC V29521;
DE 13-OCT-1998 (first entry)
DE Homo sapiens LexA-PS-1 fusion protein cDNA.
KW fusion protein; LexA; PS-1; presenilin; presenilin-1; PSP-1;
KW Alzheimer's disease; serine protease; neurodegeneration;
KW predisposition; diagnosis; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Key 2..523
FT CDS /*tag= a
FT /product= LexA-PS- fusion protein
FT EP-828003-A2.
FT 11-MAR-1998.
PD 26-AUG-1997; 306501.
PR 13-DEC-1996; US-032875.
PR 06-SEP-1996; US-025436.
PR 25-OCT-1996; US-027873.
PA (SMIK ) SMITHKLINE BEECHAM CORP.
PA (SMIK ) SMITHKLINE BEECHAM PLC.
PI Browne MJ, Clinkenbeard HE, Creasy CL, Karran EH,
PI Livi GP, Southan CD;
PI WPI: 98-161101/15.
DR P-PSDB: W56766.
DR Nucleic acids encoding human serum protease protein(s) - used for
PT diagnosing pre-disposition to Alzheimer's disease, etc.
PS Example 2; Page 17; 65pp; English.
CC The sequence is that encoding a LexA-PS-1 fusion protein which
CC was used in the cloning of PSP-1. This can be used to identify
CC modulators of serine protease activity and also to diagnose a
CC condition associated with lack of one of the serine proteases
CC or a genetic predisposition to neurodegeneration in a patient,
CC preferably predisposition to Alzheimer's disease.
SQ Sequence 732 BP; 197 A; 177 C; 184 G; 174 T;

Query Match 1.2%; Score 17; DB 1; Length 732;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 820 atctctcttgcacatccc 836
DB 131 ATCTCTCTTTGCCATCCC 147
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RESULT 12
V28875/G
ID V28875 standard; cDNA; 1029 BP.
AC V28875;
DE 28-AUG-1998 (first entry)
DE Candida antarctica lipase B c1b gene coding region.
KW Host cell; neutral metalloprotease; alkaline protease; lipase B;
KW Clb gene; ss.
OS Candida antarctica.
PN WO9812300-A1.
PD 26-MAR-1998.
PF 19-SEP-1997; DK0397.
PR 19-SEP-1996; DK-001024.
PA (NOVO ) NOVO-NORDISK AS.
PI Lehbeck J;
DR WPI; 98-217244/19.
PT New modified host cells - are modified to express reduced levels of
PT metallo-protease and alkaline protease, used to increase production
PT of heterologous protein products
PS Example 2; Page 32; 49pp; English.
CC This polynucleotide comprises the coding region of the lipase B
CC clb gene of Candida antarctica. The clb gene was isolated from a
CC C. antarctica genomic library using probes (see V28873-74) based on
CC the N-terminal amino acid sequence (see W57238) of lipase B. The
CC gene was expressed in Aspergillus oryzae IFO 4177 and JAL228, the
CC latter having both the alkaline protease alp gene (see V28870) and
CC neutral metalloprotease I Npi gene (see V28869) deleted. Clb
CC activity reached 1041 LU/g after 93 hr fermentation of JAL228,
CC compared with 575 LU/g with IFO 4177. The invention provides
CC metalloprotease- and alkaline protease-deleted yeast and fungal
CC host cells and their use for improved production of heterologous
CC protein products.
SQ Sequence 1029 BP; 183 A; 376 C; 259 G; 211 T;

Query Match 1-2%; Score 17; DB 1; Length 1029;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 ggctgcgaaagcagg 74
   |||||
Db 110 GGCTGCGAAAGCAGG 94

RESULT 13
V84576/c
ID V84576 standard; DNA; 1348 BP.
AC V84576;
DE 01-MAR-1999 (first entry)
DE Human secreted protein gene 166 clone HCE0A68.
KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
OS Homo sapiens.
PN WO9854963-A2.
PD 10-DEC-1998.
PF 04-JUN-1998; U11422.
PR 18-DEC-1997; US-070923.
PR 06-JUN-1997; US-048877.
PR 06-JUN-1997; US-048881.
PR 06-JUN-1997; US-048884.
PR 06-JUN-1997; US-048893.
PR 06-JUN-1997; US-048896.
PR 06-JUN-1997; US-048899.
PR 06-JUN-1997; US-048915.
PR 06-JUN-1997; US-048949.
PR 06-JUN-1997; US-048964.
PR 06-JUN-1997; US-048972.

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PR 06-JUN-1997; US-049020.
PR 06-JUN-1997; US-049375.
PR 05-SEP-1997; US-057628.
PR 05-SEP-1997; US-057635.
PR 05-SEP-1997; US-057644.
PR 05-SEP-1997; US-057647.
PR 05-SEP-1997; US-057650.
PR 05-SEP-1997; US-057661.
PR 05-SEP-1997; US-057667.
PR 05-SEP-1997; US-057761.
PR 05-SEP-1997; US-057764.
PR 05-SEP-1997; US-057770.
PR 05-SEP-1997; US-057775.
PR 05-SEP-1997; US-057778.
PR 06-JUN-1997; US-048875.
PR 06-JUN-1997; US-048878.
PR 06-JUN-1997; US-048882.
PR 06-JUN-1997; US-048885.
PR 06-JUN-1997; US-048894.
PR 06-JUN-1997; US-048897.
PR 06-JUN-1997; US-048900.
PR 06-JUN-1997; US-048916.
PR 06-JUN-1997; US-048962.
PR 06-JUN-1997; US-048970.
PR 06-JUN-1997; US-048974.
PR 06-JUN-1997; US-049373.
PR 05-SEP-1997; US-057584.
PR 05-SEP-1997; US-057629.
PR 05-SEP-1997; US-057642.
PR 05-SEP-1997; US-057645.
PR 05-SEP-1997; US-057648.
PR 05-SEP-1997; US-057651.
PR 05-SEP-1997; US-057662.
PR 05-SEP-1997; US-057668.
PR 05-SEP-1997; US-057762.
PR 05-SEP-1997; US-057765.
PR 05-SEP-1997; US-057771.
PR 06-JUN-1997; US-048876.
PR 06-JUN-1997; US-048880.
PR 06-JUN-1997; US-048883.
PR 06-JUN-1997; US-048892.
PR 06-JUN-1997; US-048895.
PR 06-JUN-1997; US-048898.
PR 06-JUN-1997; US-048901.
PR 06-JUN-1997; US-048917.
PR 06-JUN-1997; US-048963.
PR 06-JUN-1997; US-048971.
PR 06-JUN-1997; US-049019.
PR 06-JUN-1997; US-049374.
PR 05-SEP-1997; US-057627.
PR 05-SEP-1997; US-057634.
PR 05-SEP-1997; US-057643.
PR 05-SEP-1997; US-057646.
PR 05-SEP-1997; US-057649.
PR 05-SEP-1997; US-057654.
PR 05-SEP-1997; US-057666.
PR 05-SEP-1997; US-057760.
PR 05-SEP-1997; US-057763.
PR 05-SEP-1997; US-057769.
PR 05-SEP-1997; US-057774.
PR 05-SEP-1997; US-057777.
PA (HUMA-) HUMAN GENOME SCI INC.
PI Brewer LA, Carter KC, Dillon PJ, Ebner R, Endress GA,
PI Fan P, Feng P, Ferrie AM, Fischer CL, Florence C,
PI Florence K, Greene JM, Hu J, Kyaw H, Lafleur DW,
PI Li Y, Moore PA, Ni J, Olsen HS, Rosen CA, Ruben SM,
PI Shi Y, Soppet DR, Wei Y, Young P, Yu G, Zeng Z;
DR WPI; 99-059865/05.
DR P-ESDB; W88699.
PT New isolated human genes and the secreted polypeptides they encode -
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders

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PS Claim 4; Page 427-428; 772pp; English.
 CC The invention relates to nucleic acid sequences (V84411 to V84633)
 CC encoding human secreted proteins (W89534 to W89756). The secreted protein
 CC gene sequences are deposited with the ATCC under deposit numbers ATCC
 CC 97979, 97974, 97975, 97976, 97977, 209007, 209008, 209009, 209010,
 CC 209011, 209080, 209081, 209082, 209083, 209084, 209085, 209511. Host
 CC cells comprising recombinant vectors containing the nucleic acid
 CC sequences are used for the recombinant production of the secreted
 CC proteins. The polynucleotide and amino acid sequences are useful for are
 CC useful for preventing, treating or ameliorating medical conditions e.g.
 CC by protein or gene therapy. Pathological conditions can be also diagnosed
 CC by determining the amount of the new polypeptides in a sample or by
 CC determining the presence of mutations in the new polynucleotides.
 CC Specific uses are described for each of the polynucleotides, based on
 CC which tissues they are most highly expressed in, and include developing
 CC products for the diagnosis or treatment of cancer, neurodegenerative
 CC disorders, developmental abnormalities and foetal deficiencies, blood
 CC disorders, tumours, leukemias, diseases of the immune system, autoimmune
 CC diseases, hepatic and renal disease, lymphomas, inflammation, allergies,
 CC ischemic shock, Alzheimer's and cognitive disorders, schizophrenia,
 CC restenosis, prostate diseases, obesity, disorders involving osteoclasts
 CC such as osteoporosis, arthritis or malignancies, diseases of testes, lung
 CC or thymus, digestive/endocrine disorders, infections and AIDS. The
 CC polypeptides are also useful for identifying their binding partners.
 CC The present sequence represents a gene encoding a human secreted protein
 CC (see descriptor line for gene number and clone identification).
 CC Sequence 1348 BP; 286 A; 374 C; 388 G; 292 T;

Query Match 1.2%; Score 17; DB 1; Length 1348;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 641 tgaccggcgatcggtg 657
 Db 24 TGACCGCGCGCATCGTG 8

RESULT 14
 V29523
 ID V29523 standard; cDNA; 1503 BP.
 AC V29523; 1998 (first entry)
 DT Homo sapiens PSP1 clone.
 DE PS-1; presenilin; presenilin-1; PSP-1; Alzheimer's disease;
 KW serine protease; neurodegeneration; predisposition; diagnosis; ss.
 OS Homo sapiens.

Key Location/Qualifiers
 FT 1..1272
 CDS /product= PSP1 fragment
 FT EP-828003-A2.
 PN 11-MAR-1998.
 PD 26-AUG-1997; 306501.
 PF 13-DEC-1996; US-032875.
 PR 06-SEP-1996; US-025436.
 PR 25-OCT-1996; US-027873.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PI Browne MJ, Clinkenbeard HE, Creasy CL, Karman EH,
 PI Livi GP, Southan CD;
 PI WPI: 98-161101/15.
 DR P-PSDB; W56768.
 PT Nucleic acids encoding human serum protease protein(s) - used for
 PT diagnosing pre-disposition to Alzheimer's disease, etc.
 PS Example 2; Page 19-20; 65pp; English.
 CC The sequence is that of an isolated cDNA clone encoding at least
 CC part of the serine protease PSP1. This can be used to identify
 CC modulators of serine protease activity and also to diagnose a
 CC condition associated with lack of one of the serine proteases
 CC or a genetic predisposition to neurodegeneration in a patient,
 CC preferably predisposition to Alzheimer's disease.
 CC Sequence 1503 BP; 329 A; 405 C; 448 G; 321 T;

Query Match 1.2%; Score 17; DB 1; Length 1503;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 820 atctcctttgcatccc 836
 Db 976 ATCTCCTTTGCCATCCC 992

RESULT 15
 V29522
 ID V29522 standard; cDNA; 1787 BP.
 AC V29522;
 DT 13-OCT-1998 (first entry)
 DE Homo sapiens PSP1 clone.
 KW PS-1; presenilin; presenilin-1; PSP-1; Alzheimer's disease;
 KW serine protease; neurodegeneration; predisposition; diagnosis; ss.
 OS Homo sapiens.
 Key Location/Qualifiers
 FT 1..972
 CDS /product= PSP1 fragment
 FT EP-828003-A2.
 PN 11-MAR-1998.
 PD 26-AUG-1997; 306501.
 PF 13-DEC-1996; US-032875.
 PR 06-SEP-1996; US-025436.
 PR 25-OCT-1996; US-027873.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PI Browne MJ, Clinkenbeard HE, Creasy CL, Karman EH,
 PI Livi GP, Southan CD;
 PI WPI: 98-161101/15.
 DR P-PSDB; W56767.
 PT Nucleic acids encoding human serum protease protein(s) - used for
 PT diagnosing pre-disposition to Alzheimer's disease, etc.
 PS Example 2; Page 18; 65pp; English.
 CC The sequence is that of an isolated cDNA clone encoding at least
 CC part of the serine protease PSP1. This can be used to identify
 CC modulators of serine protease activity and also to diagnose a
 CC condition associated with lack of one of the serine proteases
 CC or a genetic predisposition to neurodegeneration in a patient,
 CC preferably predisposition to Alzheimer's disease.
 CC Sequence 1787 BP; 392 A; 480 C; 498 G; 417 T;

Query Match 1.2%; Score 17; DB 1; Length 1787;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 820 atctcctttgcatccc 836
 Db 1048 ATCTCCTTTGCCATCCC 1064

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Perfect score: 1395									
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Scoring table: OLIGO_NUC									
Searched: Gapop 60.0 , Gapext 60.0									
Word size : 0									
Total number of hits satisfying chosen parameters: 428588									
Minimum DB seq length: 0									
Maximum DB seq length: 1000000									
Post-processing: Listing first 1000 summaries									
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*									
3: /cgn2_6/ptodata/2/ina/5C_COMB.seq.*									
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5: /cgn2_6/ptodata/2/ina/6_COMB.seq.*									
6: /cgn2_6/ptodata/2/ina/PCTUS9_COMB.seq.*									
7: /cgn2_6/ptodata/2/ina/backfiles1.seq.*									
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SUMMARIES									
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C 1	17	1.2	49377	2	US-08-764-233A-1	Sequence 1, Appli			
C 2	16	1.1	76	6	PCT-US91-02942-27	Sequence 27, Appl			
C 3	16	1.1	388	1	US-08-171-385-10	Sequence 10, Appl			
C 4	16	1.1	894	2	US-08-534-910B-4	Sequence 4, Appli			
C 5	16	1.1	929	5	US-08-860-368B-4	Sequence 4, Appli			
C 6	16	1.1	1155	5	US-08-860-368B-19	Sequence 19, Appl			
C 7	16	1.1	1158	5	US-08-860-368B-1	Sequence 1, Appli			
C 8	16	1.1	1288	1	US-08-142-897-4	Sequence 4, Appli			
C 9	16	1.1	1479	1	US-08-476-008-68	Sequence 68, Appl			
C 10	16	1.1	1479	2	US-08-306-063-68	Sequence 68, Appl			
C 11	16	1.1	1479	2	US-08-833-485-68	Sequence 8, Appli			
C 12	16	1.1	2061	1	US-08-204-656B-9	Sequence 9, Appli			
C 13	16	1.1	2061	1	US-08-470-702-5	Sequence 5, Appli			
C 14	16	1.1	2061	1	US-08-467-831-5	Sequence 7, Appli			
C 15	16	1.1	2157	3	US-08-132-990A-7	Sequence 9, Appli			
C 16	16	1.1	2157	6	PCT-US92-09382-7	Sequence 9, Appli			
C 17	16	1.1	4474	2	US-08-480-547A-9	Sequence 9, Appli			
C 18	16	1.1	4474	2	US-08-250-847B-9	Sequence 9, Appli			
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C 20	16	1.1	4474	6	PCT-US94-06066-9	Sequence 9, Appli			
C 21	16	1.1	5541	2	US-08-920-812-20	Sequence 20, Appl			
C 22	16	1.1	5541	2	US-08-920-812-20	Sequence 20, Appl			
C 23	16	1.1	5541	2	US-08-921-177-20	Sequence 20, Appl			
C 24	16	1.1	5541	2	US-08-362-577C-20	Sequence 20, Appl			
C 25	16	1.1	5541	3	US-08-920-828-20	Sequence 20, Appl			
C 26	16	1.1	8378	6	PCT-US91-09055-1	Sequence 1, Appli			
C 27	16	1.1	9432	1	US-08-277-231A-1	Sequence 1, Appli			
C 28	16	1.1	9432	3	US-08-473-750-4	Sequence 4, Appli			
C 29	16	1.1	9432	4	US-08-477-326-4	Sequence 4, Appli			
C 30	16	1.1	14255	1	US-08-320-559-1	Sequence 1, Appli			
C 31	16	1.1	14255	1	US-08-327-392-1	Sequence 1, Appli			
C 32	16	1.1	14255	2	US-08-306-691B-55	Sequence 55, Appl			
C 33	16	1.1	14255	6	PCT-US94-04496-1	Sequence 1, Appli			
C 34	15	1.1	570	1	US-07-963-331D-2	Sequence 2, Appli			
C 35	15	1.1	573	4	US-07-963-331D-1	Sequence 1, Appli			
C 36	15	1.1	804	4	US-08-611-880-4	Sequence 15, Appl			
C 37	15	1.1	1434	3	US-08-770-548-15	Sequence 11, Appl			
C 38	15	1.1	1850	3	US-08-245-758-11	Sequence 11, Appl			
C 39	15	1.1	1850	4	US-08-810-635A-1	Sequence 11, Appl			
C 40	15	1.1	1650	6	PCT-US95-05134-11	Sequence 33, Appl			
C 41	15	1.1	1677	4	US-08-989-107-33	Sequence 11, Appl			
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C 44	15	1.1	1767	1	US-08-399-646-1	Sequence 1, Appli			
C 45	15	1.1	1767	2	US-08-607-321-1	Sequence 1, Appli			
C 46	15	1.1	1767	3	US-08-961-240-1	Sequence 1, Appli			
C 47	15	1.1	1770	3	US-08-605-501-1	Sequence 3, Appli			
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C 49	15	1.1	1930	1	US-08-980-060-1	Sequence 1, Appli			
C 50	15	1.1	1949	4	US-07-982-112-1	Sequence 1, Appli			
C 51	15	1.1	1949	4	US-08-540-804-1	Sequence 1, Appli			
C 52	15	1.1	1949	4	US-08-218-265-1	Sequence 1, Appli			
C 53	15	1.1	1988	2	US-08-469-202-26	Sequence 26, Appl			
C 54	15	1.1	1988	4	US-08-484-434C-33	Sequence 33, Appl			
C 55	15	1.1	2000	2	US-08-469-202-25	Sequence 25, Appl			
C 56	15	1.1	2000	4	US-08-484-434C-32	Sequence 32, Appl			
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C 97	15	1.1	3809	4	US-08-480-751-3	Sequence 3, Appli			
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C 99	15	1.1	3809	5	US-08-353-784-3	Sequence 3, Appli			

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c 101	15	1.1	3921	4	US-08-587-680A-3	Sequence 3, Appl	c 174	14	1.0	78	1	US-08-411-796-176	Sequence 176, App
c 102	15	1.1	4086	1	US-08-313-181-1	Sequence 1, Appl	c 175	14	1.0	78	1	US-08-411-796-177	Sequence 177, App
c 103	15	1.1	4131	1	US-08-485-588-4	Sequence 4, Appl	c 176	14	1.0	78	6	PCT-US93-11198-61	Sequence 61, Appl
c 104	15	1.1	4131	2	US-08-484-565-4	Sequence 4, Appl	c 177	14	1.0	78	6	PCT-US93-11198-172	Sequence 172, App
c 105	15	1.1	4131	3	US-08-480-751-4	Sequence 4, Appl	c 178	14	1.0	78	6	PCT-US93-11198-173	Sequence 173, App
c 106	15	1.1	4131	4	US-08-943-986-4	Sequence 4, Appl	c 179	14	1.0	78	6	PCT-US93-11198-174	Sequence 174, App
c 107	15	1.1	4131	5	US-08-353-784-4	Sequence 4, Appl	c 180	14	1.0	78	6	PCT-US93-11198-175	Sequence 175, App
c 108	15	1.1	4440	1	US-08-200-016-4	Sequence 4, Appl	c 181	14	1.0	78	6	PCT-US93-11198-176	Sequence 176, App
c 109	15	1.1	5006	1	US-08-485-588-2	Sequence 2, Appl	c 182	14	1.0	78	6	PCT-US93-11198-177	Sequence 177, App
c 110	15	1.1	5006	2	US-08-484-565-2	Sequence 2, Appl	c 183	14	1.0	146	3	US-08-447-173A-13	Sequence 13, Appl
c 111	15	1.1	5006	3	US-08-480-751-2	Sequence 2, Appl	c 184	14	1.0	159	2	US-08-485-455D-78	Sequence 78, Appl
c 112	15	1.1	5006	4	US-08-943-986-2	Sequence 2, Appl	c 185	14	1.0	159	4	US-08-482-130C-78	Sequence 78, Appl
c 113	15	1.1	5006	5	US-08-353-784-2	Sequence 2, Appl	c 186	14	1.0	159	4	US-08-484-211C-78	Sequence 78, Appl
c 114	15	1.1	5125	1	US-08-094-949A-4	Sequence 4, Appl	c 187	14	1.0	159	4	US-08-484-211C-78	Sequence 78, Appl
c 115	15	1.1	5125	6	PCT-US96-09319-4	Sequence 4, Appl	c 188	14	1.0	219	6	PCT-US95-14442A-78	Patent No. 5217896
c 116	15	1.1	5275	1	US-08-485-588-1	Sequence 1, Appl	c 189	14	1.0	240	7	5177308-2	Patent No. 5177308
c 117	15	1.1	5275	2	US-08-484-565-1	Sequence 1, Appl	c 190	14	1.0	243	4	US-08-505-218-7	Sequence 7, Appl
c 118	15	1.1	5275	3	US-08-480-751-1	Sequence 1, Appl	c 191	14	1.0	315	1	US-08-081-539-89	Sequence 89, Appl
c 119	15	1.1	5275	4	US-08-943-986-1	Sequence 1, Appl	c 192	14	1.0	315	1	US-08-466-647-89	Sequence 89, Appl
c 120	15	1.1	5275	5	US-08-353-784-1	Sequence 1, Appl	c 193	14	1.0	323	3	US-08-506-864A-4	Sequence 4, Appl
c 121	15	1.1	5992	3	US-08-475-891A-3	Sequence 3, Appl	c 194	14	1.0	323	4	US-08-851-968-4	Sequence 4, Appl
c 122	15	1.1	6256	3	US-08-475-891A-1	Sequence 1, Appl	c 195	14	1.0	330	1	US-08-081-539-84	Sequence 84, Appl
c 123	15	1.1	6256	4	US-08-567-375-1	Sequence 1, Appl	c 196	14	1.0	330	1	US-08-466-647-84	Sequence 84, Appl
c 124	15	1.1	6256	4	US-08-587-680A-1	Sequence 1, Appl	c 197	14	1.0	333	1	US-08-411-795B-106	Sequence 106, App
c 125	15	1.1	7451	2	US-08-684-672-23	Sequence 23, Appl	c 198	14	1.0	333	1	US-08-411-795B-107	Sequence 107, App
c 126	15	1.1	8051	4	US-08-576-626A-2	Sequence 2, Appl	c 199	14	1.0	333	1	US-08-411-795B-108	Sequence 108, App
c 127	15	1.1	9493	4	US-08-639-857-23	Sequence 23, Appl	c 200	14	1.0	333	1	US-08-411-795B-109	Sequence 109, App
c 128	15	1.1	49472	2	US-08-614-770A-1	Sequence 1, Appl	c 201	14	1.0	333	1	US-08-411-795B-110	Sequence 110, App
c 129	14	1.0	21	1	US-08-009-263C-55	Sequence 55, Appl	c 202	14	1.0	333	1	US-08-411-795B-111	Sequence 111, App
c 130	14	1.0	24	1	US-08-411-795B-199	Sequence 199, App	c 203	14	1.0	333	1	US-08-411-795B-112	Sequence 112, App
c 131	14	1.0	24	6	PCT-US93-11198-199	Sequence 199, App	c 204	14	1.0	333	1	US-08-411-795B-113	Sequence 113, App
c 132	14	1.0	32	1	US-08-530-492B-81	Sequence 81, Appl	c 205	14	1.0	333	1	US-08-411-795B-116	Sequence 116, App
c 133	14	1.0	36	1	US-08-319-492B-228	Sequence 228, App	c 206	14	1.0	333	1	US-08-411-795B-117	Sequence 117, App
c 134	14	1.0	39	2	US-08-481-003-14	Sequence 14, Appl	c 207	14	1.0	333	1	US-08-411-795B-118	Sequence 118, App
c 135	14	1.0	54	1	US-07-982-712-18	Sequence 18, Appl	c 208	14	1.0	333	2	US-08-469-319A-106	Sequence 106, App
c 136	14	1.0	54	1	US-07-875-758-5	Sequence 5, Appl	c 209	14	1.0	333	2	US-08-469-319A-107	Sequence 107, App
c 137	14	1.0	60	1	US-08-411-796-62	Sequence 62, Appl	c 210	14	1.0	333	2	US-08-469-319A-108	Sequence 108, App
c 138	14	1.0	60	1	US-08-411-796-178	Sequence 178, App	c 211	14	1.0	333	2	US-08-469-319A-109	Sequence 109, App
c 139	14	1.0	60	6	PCT-US93-11198-62	Sequence 62, Appl	c 212	14	1.0	333	2	US-08-469-319A-110	Sequence 110, App
c 140	14	1.0	60	6	PCT-US93-11198-178	Sequence 178, App	c 213	14	1.0	333	2	US-08-469-319A-111	Sequence 111, App
c 141	14	1.0	64	1	US-08-081-539-15	Sequence 15, Appl	c 214	14	1.0	333	2	US-08-469-319A-112	Sequence 112, App
c 142	14	1.0	64	1	US-08-081-539-15	Sequence 15, Appl	c 215	14	1.0	333	2	US-08-469-319A-113	Sequence 113, App
c 143	14	1.0	64	1	US-08-466-647-15	Sequence 15, Appl	c 216	14	1.0	333	2	US-08-469-319A-116	Sequence 116, App
c 144	14	1.0	64	1	US-08-466-647-16	Sequence 16, Appl	c 217	14	1.0	333	2	US-08-469-319A-117	Sequence 117, App
c 145	14	1.0	64	1	US-08-411-795B-8	Sequence 8, Appl	c 218	14	1.0	333	2	US-08-469-319A-118	Sequence 118, App
c 146	14	1.0	64	1	US-08-411-795B-9	Sequence 9, Appl	c 219	14	1.0	336	1	US-08-081-539-77	Sequence 77, Appl
c 147	14	1.0	64	1	US-08-411-795B-142	Sequence 142, App	c 220	14	1.0	336	1	US-08-081-539-79	Sequence 79, Appl
c 148	14	1.0	64	1	US-08-411-795B-143	Sequence 143, App	c 221	14	1.0	336	1	US-08-081-539-80	Sequence 80, Appl
c 149	14	1.0	64	1	US-08-411-796-8	Sequence 8, Appl	c 222	14	1.0	336	1	US-08-081-539-81	Sequence 81, Appl
c 150	14	1.0	64	1	US-08-411-796-9	Sequence 9, Appl	c 223	14	1.0	336	1	US-08-081-539-82	Sequence 82, Appl
c 151	14	1.0	64	2	US-08-469-319A-8	Sequence 8, Appl	c 224	14	1.0	336	1	US-08-081-539-83	Sequence 83, Appl
c 152	14	1.0	64	2	US-08-469-319A-9	Sequence 9, Appl	c 225	14	1.0	336	1	US-08-081-539-85	Sequence 85, Appl
c 153	14	1.0	64	2	US-08-469-319A-142	Sequence 142, App	c 226	14	1.0	336	1	US-08-081-539-86	Sequence 86, Appl
c 154	14	1.0	64	2	US-08-469-319A-143	Sequence 143, App	c 227	14	1.0	336	1	US-08-081-539-87	Sequence 87, Appl
c 155	14	1.0	64	6	PCT-US93-11198-8	Sequence 8, Appl	c 228	14	1.0	336	1	US-08-081-539-88	Sequence 88, Appl
c 156	14	1.0	64	6	PCT-US93-11198-9	Sequence 9, Appl	c 229	14	1.0	336	1	US-08-081-539-90	Sequence 90, Appl
c 157	14	1.0	71	1	US-08-081-539-11	Sequence 11, Appl	c 230	14	1.0	336	1	US-08-081-539-91	Sequence 91, Appl
c 158	14	1.0	71	1	US-08-081-539-12	Sequence 12, Appl	c 231	14	1.0	336	1	US-08-081-539-96	Sequence 96, Appl
c 159	14	1.0	71	1	US-08-466-647-11	Sequence 11, Appl	c 232	14	1.0	336	1	US-08-081-539-97	Sequence 97, Appl
c 160	14	1.0	71	1	US-08-466-647-12	Sequence 12, Appl	c 233	14	1.0	336	1	US-08-081-539-100	Sequence 100, App
c 161	14	1.0	71	1	US-08-411-795B-136	Sequence 136, App	c 234	14	1.0	336	1	US-08-081-539-101	Sequence 101, App
c 162	14	1.0	71	1	US-08-411-795B-137	Sequence 137, App	c 235	14	1.0	336	1	US-08-466-647-77	Sequence 77, Appl
c 163	14	1.0	71	1	US-08-411-796-136	Sequence 136, App	c 236	14	1.0	336	1	US-08-466-647-79	Sequence 79, Appl
c 164	14	1.0	71	1	US-08-411-796-137	Sequence 137, App	c 237	14	1.0	336	1	US-08-466-647-80	Sequence 80, Appl
c 165	14	1.0	71	2	US-08-469-319A-136	Sequence 136, App	c 238	14	1.0	336	1	US-08-466-647-81	Sequence 81, Appl
c 166	14	1.0	71	2	US-08-469-319A-137	Sequence 137, App	c 239	14	1.0	336	1	US-08-466-647-82	Sequence 82, Appl
c 167	14	1.0	71	6	PCT-US93-11198-136	Sequence 136, App	c 240	14	1.0	336	1	US-08-466-647-83	Sequence 83, Appl
c 168	14	1.0	71	6	PCT-US93-11198-137	Sequence 137, App	c 241	14	1.0	336	1	US-08-466-647-85	Sequence 85, Appl
c 169	14	1.0	78	1	US-08-411-796-61	Sequence 61, Appl	c 242	14	1.0	336	1	US-08-466-647-86	Sequence 86, Appl
c 170	14	1.0	78	1	US-08-411-796-172	Sequence 172, App	c 243	14	1.0	336	1	US-08-466-647-87	Sequence 87, Appl
c 171	14	1.0	78	1	US-08-411-796-173	Sequence 173, App	c 244	14	1.0	336	1	US-08-466-647-88	Sequence 88, Appl
c 172	14	1.0	78	1	US-08-411-796-174	Sequence 174, App	c 245	14	1.0	336	1	US-08-466-647-90	Sequence 90, Appl

246	14	1.0	336	1	US-08-466-647-91	Sequence 91, Appl	c 319	14	1.0	485	4	US-08-997-080-106	Sequence 106, App
247	14	1.0	336	1	US-08-466-647-96	Sequence 96, Appl	c 320	14	1.0	485	4	US-08-997-362-41	Sequence 41, Appl
248	14	1.0	336	1	US-08-466-647-97	Sequence 97, Appl	c 321	14	1.0	485	4	US-08-997-362-106	Sequence 106, App
249	14	1.0	336	1	US-08-466-647-100	Sequence 100, Appl	c 322	14	1.0	485	5	US-08-873-970-41	Sequence 41, Appl
250	14	1.0	336	1	US-08-466-647-101	Sequence 101, Appl	c 323	14	1.0	485	5	US-08-873-970-106	Sequence 106, App
251	14	1.0	339	1	US-08-081-539-92	Sequence 92, Appl	c 324	14	1.0	486	3	US-08-858-767-27	Sequence 27, Appl
252	14	1.0	339	1	US-08-081-539-93	Sequence 93, Appl	c 325	14	1.0	486	3	US-08-863-028-27	Sequence 27, Appl
253	14	1.0	339	1	US-08-081-539-102	Sequence 102, Appl	c 326	14	1.0	568	4	US-08-505-218-1	Sequence 1, Appl
254	14	1.0	339	1	US-08-081-539-103	Sequence 103, Appl	c 327	14	1.0	568	4	US-08-505-218-12	Sequence 12, Appl
255	14	1.0	339	1	US-08-466-647-92	Sequence 92, Appl	c 328	14	1.0	600	7	5198345-4	Patent No. 5198345
256	14	1.0	339	1	US-08-466-647-93	Sequence 93, Appl	c 329	14	1.0	602	1	PCT-US94-04174-27	Sequence 27, Appl
257	14	1.0	339	1	US-08-466-647-102	Sequence 102, Appl	c 330	14	1.0	647	6	US-08-403-388-4	Sequence 4, Appl
258	14	1.0	339	1	US-08-466-647-103	Sequence 103, Appl	c 331	14	1.0	687	1	US-08-658-378-4	Sequence 4, Appl
259	14	1.0	339	1	US-08-411-795B-122	Sequence 122, Appl	c 332	14	1.0	687	2	US-08-618-911-1	Sequence 1, Appl
260	14	1.0	339	1	US-08-411-795B-123	Sequence 123, Appl	c 333	14	1.0	723	3	US-08-512-955-3	Sequence 3, Appl
261	14	1.0	339	1	US-08-411-795B-124	Sequence 124, Appl	c 334	14	1.0	729	4	US-08-471-969-12	Sequence 12, Appl
262	14	1.0	339	1	US-08-411-795B-125	Sequence 125, Appl	c 335	14	1.0	748	2	US-08-471-969-12	Sequence 12, Appl
263	14	1.0	339	1	US-08-411-795B-398	Sequence 398, Appl	c 336	14	1.0	748	2	US-08-384-137-12	Sequence 12, Appl
264	14	1.0	339	1	US-08-411-795B-399	Sequence 399, Appl	c 337	14	1.0	748	3	US-08-470-006A-12	Sequence 12, Appl
265	14	1.0	339	1	US-08-411-796-68	Sequence 68, Appl	c 338	14	1.0	748	5	US-08-691-563C-12	Sequence 12, Appl
266	14	1.0	339	1	US-08-411-796-216	Sequence 216, Appl	c 339	14	1.0	762	2	US-08-532-390-40	Sequence 40, Appl
267	14	1.0	339	1	US-08-411-796-220	Sequence 220, Appl	c 340	14	1.0	783	2	US-08-256-964A-16	Sequence 16, Appl
268	14	1.0	339	2	US-08-469-319A-122	Sequence 122, Appl	c 341	14	1.0	807	1	US-08-165-315D-1	Sequence 1, Appl
269	14	1.0	339	2	US-08-469-319A-123	Sequence 123, Appl	c 342	14	1.0	824	4	US-08-922-170B-12	Sequence 12, Appl
270	14	1.0	339	2	US-08-469-319A-124	Sequence 124, Appl	c 343	14	1.0	846	1	US-08-165-315D-2	Sequence 2, Appl
271	14	1.0	339	2	US-08-469-319A-398	Sequence 398, Appl	c 344	14	1.0	850	6	PCT-US95-14442A-102	Sequence 102, App
272	14	1.0	339	6	PCT-US93-11198-68	Sequence 68, Appl	c 345	14	1.0	853	1	US-08-008-216-16	Sequence 16, Appl
273	14	1.0	339	6	PCT-US93-11198-216	Sequence 216, Appl	c 346	14	1.0	853	1	US-08-459-569-16	Sequence 16, Appl
274	14	1.0	339	6	PCT-US93-11198-220	Sequence 220, Appl	c 347	14	1.0	853	2	US-08-458-831-16	Sequence 16, Appl
275	14	1.0	340	1	US-08-411-795B-408	Sequence 408, Appl	c 348	14	1.0	858	3	US-08-796-676-2	Sequence 2, Appl
276	14	1.0	340	2	US-08-469-319A-408	Sequence 408, Appl	c 349	14	1.0	912	4	US-08-993-228-7	Sequence 7, Appl
277	14	1.0	342	1	US-08-081-539-78	Sequence 78, Appl	c 350	14	1.0	913	1	US-08-109-391A-1	Sequence 1, Appl
278	14	1.0	342	1	US-08-466-647-78	Sequence 78, Appl	c 351	14	1.0	913	4	US-08-459-018A-1	Sequence 1, Appl
279	14	1.0	359	4	US-08-687-080-65	Sequence 65, Appl	c 352	14	1.0	913	4	US-08-460-429A-1	Sequence 1, Appl
280	14	1.0	360	1	US-08-081-539-94	Sequence 94, Appl	c 353	14	1.0	925	2	US-08-544-900-3	Sequence 3, Appl
281	14	1.0	360	1	US-08-081-539-99	Sequence 99, Appl	c 354	14	1.0	925	6	PCT-US95-07874-2	Sequence 2, Appl
282	14	1.0	360	1	US-08-466-647-94	Sequence 94, Appl	c 355	14	1.0	950	7	5177308-3	Patent No. 5177308
283	14	1.0	360	1	US-08-466-647-99	Sequence 99, Appl	c 356	14	1.0	957	1	US-07-745-206A-16	Sequence 16, Appl
284	14	1.0	378	1	US-08-081-539-95	Sequence 95, Appl	c 357	14	1.0	957	3	US-08-311-363-16	Sequence 16, Appl
285	14	1.0	378	1	US-08-466-647-95	Sequence 95, Appl	c 358	14	1.0	972	1	US-08-276-887A-12	Sequence 12, Appl
286	14	1.0	381	6	PCT-US96-03916-14	Sequence 14, Appl	c 359	14	1.0	1029	1	US-08-008-216-15	Sequence 15, Appl
287	14	1.0	408	1	US-08-081-539-104	Sequence 104, Appl	c 360	14	1.0	1029	2	US-08-459-569-15	Sequence 15, Appl
288	14	1.0	408	1	US-08-466-647-104	Sequence 104, Appl	c 361	14	1.0	1029	2	US-08-458-831-15	Sequence 15, Appl
289	14	1.0	408	1	US-08-411-795B-144	Sequence 144, Appl	c 362	14	1.0	1060	3	US-08-385-335A-14	Sequence 14, Appl
290	14	1.0	408	1	US-08-411-796-144	Sequence 144, Appl	c 363	14	1.0	1083	4	US-08-313-866-1	Sequence 1, Appl
291	14	1.0	408	2	US-08-192-299B-10	Sequence 10, Appl	c 364	14	1.0	1103	2	US-08-183-214-9	Sequence 9, Appl
292	14	1.0	408	2	US-08-191-973B-10	Sequence 10, Appl	c 365	14	1.0	1125	4	US-07-928-462-1	Sequence 1, Appl
293	14	1.0	408	3	US-08-469-319A-144	Sequence 144, Appl	c 366	14	1.0	1138	4	US-08-993-228-5	Sequence 5, Appl
294	14	1.0	408	3	US-08-470-775-10	Sequence 10, Appl	c 367	14	1.0	1247	1	US-08-278-729A-32	Sequence 32, Appl
295	14	1.0	408	4	US-08-470-509-10	Sequence 10, Appl	c 368	14	1.0	1247	1	US-08-155-343A-32	Sequence 32, Appl
296	14	1.0	408	4	US-08-559-009-10	Sequence 10, Appl	c 369	14	1.0	1247	2	US-08-406-672-32	Sequence 32, Appl
297	14	1.0	408	6	PCT-US93-11198-144	Sequence 144, Appl	c 370	14	1.0	1247	2	US-08-643-563A-32	Sequence 32, Appl
298	14	1.0	414	1	US-08-081-539-120	Sequence 120, Appl	c 371	14	1.0	1247	2	US-08-643-763A-32	Sequence 32, Appl
299	14	1.0	414	1	US-08-081-539-121	Sequence 121, Appl	c 372	14	1.0	1247	2	US-08-462-623-32	Sequence 32, Appl
300	14	1.0	414	1	US-08-466-647-120	Sequence 120, Appl	c 373	14	1.0	1247	2	US-08-451-953A-32	Sequence 32, Appl
301	14	1.0	414	1	US-08-466-647-121	Sequence 121, Appl	c 374	14	1.0	1247	3	US-08-445-468A-32	Sequence 32, Appl
302	14	1.0	414	1	US-08-411-795B-147	Sequence 147, Appl	c 375	14	1.0	1247	4	US-08-461-397A-32	Sequence 32, Appl
303	14	1.0	414	1	US-08-411-795B-148	Sequence 148, Appl	c 376	14	1.0	1247	4	US-08-912-088-32	Sequence 32, Appl
304	14	1.0	414	1	US-08-411-796-147	Sequence 147, Appl	c 377	14	1.0	1247	6	PCT-US93-07231-32	Sequence 32, Appl
305	14	1.0	414	1	US-08-411-796-148	Sequence 148, Appl	c 378	14	1.0	1247	6	PCT-US93-07190-32	Sequence 32, Appl
306	14	1.0	414	2	US-08-469-319A-147	Sequence 147, Appl	c 379	14	1.0	1247	6	PCT-US93-08742-32	Sequence 32, Appl
307	14	1.0	414	2	US-08-469-319A-148	Sequence 148, Appl	c 380	14	1.0	1247	6	PCT-US93-08808-32	Sequence 32, Appl
308	14	1.0	414	6	PCT-US93-11198-147	Sequence 147, Appl	c 381	14	1.0	1247	6	PCT-US93-08885-32	Sequence 32, Appl
309	14	1.0	414	6	PCT-US93-11198-148	Sequence 148, Appl	c 382	14	1.0	1255	2	US-08-518-878B-38	Sequence 38, Appl
310	14	1.0	419	3	US-08-482-013-61	Sequence 61, Appl	c 383	14	1.0	1255	2	US-08-294-522B-38	Sequence 38, Appl
311	14	1.0	419	3	US-08-482-279-61	Sequence 61, Appl	c 384	14	1.0	1255	3	US-08-470-868A-38	Sequence 38, Appl
312	14	1.0	419	3	US-08-342-268-61	Sequence 61, Appl	c 385	14	1.0	1280	1	US-08-027-986-3	Sequence 3, Appl
313	14	1.0	421	2	US-08-486-013-44	Sequence 44, Appl	c 386	14	1.0	1290	7	5182195-14	Patent No. 5182195
314	14	1.0	421	3	US-08-482-279-44	Sequence 44, Appl	c 387	14	1.0	1299	1	US-08-453-472-3	Sequence 3, Appl
315	14	1.0	421	3	US-08-342-268-44	Sequence 44, Appl	c 388	14	1.0	1299	1	US-08-038-948-3	Sequence 3, Appl
316	14	1.0	450	4	US-08-387-942C-32	Sequence 32, Appl	c 389	14	1.0	1299	1	US-08-453-953-3	Sequence 3, Appl
317	14	1.0	456	2	US-08-450-945-70	Sequence 70, Appl	c 390	14	1.0	1299	4	US-08-862-903-3	Sequence 3, Appl
318	14	1.0	485	4	US-08-997-080-41	Sequence 41, Appl	c 391	14	1.0	1299	4	US-08-862-903-3	Sequence 3, Appl

392	14	1.0	1299	4	US-08-484-158B-60	Sequence 60, Appl	465	14	1.0	1970	5	US-08-938-548B-1	Sequence 1, Appl
c 393	14	1.0	1307	1	US-07-968-971A-6	Sequence 6, Appl	466	14	1.0	1971	4	US-08-818-253-7	Sequence 7, Appl
c 394	14	1.0	1307	1	US-08-142-473A-8	Sequence 8, Appl	467	14	1.0	1987	2	US-08-722-001-26	Sequence 26, Appl
c 395	14	1.0	1307	1	US-08-424-406-12	Sequence 13, Appl	468	14	1.0	1988	3	US-08-712-948-8	Sequence 8, Appl
c 396	14	1.0	1307	2	US-08-464-523B-11	Sequence 11, Appl	469	14	1.0	1997	2	US-08-722-001-27	Sequence 27, Appl
c 397	14	1.0	1307	2	US-08-469-203A-8	Sequence 8, Appl	470	14	1.0	2004	2	US-08-722-001-11	Sequence 11, Appl
c 398	14	1.0	1307	2	US-08-469-203A-8	Sequence 8, Appl	c 471	14	1.0	2019	1	US-08-254-357-3	Sequence 3, Appl
c 399	14	1.0	1327	1	US-08-165-315B-1	Sequence 2, Appl	472	14	1.0	2028	1	US-08-295-814E-1	Sequence 1, Appl
c 400	14	1.0	1335	1	US-08-440-377A-2	Sequence 3, Appl	473	14	1.0	2028	6	PCT-US93-01959-1	Sequence 1, Appl
c 401	14	1.0	1335	2	US-08-687-852-2	Sequence 2, Appl	474	14	1.0	2049	6	US-08-465-590-5	Sequence 5, Appl
c 402	14	1.0	1356	1	US-08-426-169-3	Sequence 3, Appl	475	14	1.0	2049	6	PCT-US95-09345-4	Sequence 4, Appl
c 403	14	1.0	1356	6	PCT-US95-09470-3	Sequence 3, Appl	476	14	1.0	2057	2	US-08-450-945-57	Sequence 57, Appl
c 404	14	1.0	1357	4	US-08-546-117-8	Sequence 8, Appl	477	14	1.0	2085	3	US-08-961-917-8	Sequence 8, Appl
c 405	14	1.0	1373	7	5514590-3	Patent No. 5514590	478	14	1.0	2085	3	US-08-961-917-8	Sequence 8, Appl
c 406	14	1.0	1378	1	US-08-075-533-20	Sequence 20, Appl	479	14	1.0	2166	4	US-08-317-401E-3	Sequence 3, Appl
c 407	14	1.0	1378	4	US-08-948-176-20	Sequence 20, Appl	480	14	1.0	2172	1	US-07-982-712-1	Sequence 1, Appl
c 408	14	1.0	1378	6	PCT-US91-09160-20	Sequence 20, Appl	c 481	14	1.0	2199	1	US-08-146-602B-5	Sequence 5, Appl
c 409	14	1.0	1389	2	US-08-702-344-20	Sequence 20, Appl	c 482	14	1.0	2217	2	US-08-543-881-1	Sequence 1, Appl
c 410	14	1.0	1412	4	US-08-948-176-23	Sequence 23, Appl	483	14	1.0	2217	2	US-08-291-239-1	Sequence 1, Appl
c 411	14	1.0	1434	4	US-08-503-801-2	Sequence 2, Appl	484	14	1.0	2217	6	PCT-US94-00119-1	Sequence 1, Appl
c 412	14	1.0	1440	1	US-07-978-892A-1	Sequence 1, Appl	485	14	1.0	2217	6	PCT-US95-10579-1	Sequence 1, Appl
c 413	14	1.0	1463	3	US-08-588-983-6	Sequence 6, Appl	c 486	14	1.0	2220	3	US-08-617-801A-1	Sequence 1, Appl
c 414	14	1.0	1463	3	US-08-588-976-6	Sequence 6, Appl	c 487	14	1.0	2232	1	US-08-179-481-97	Sequence 97, Appl
c 415	14	1.0	1485	4	US-08-874-186-41	Sequence 41, Appl	c 488	14	1.0	2292	3	US-08-889-711-1	Sequence 1, Appl
c 416	14	1.0	1493	3	US-08-820-170A-9	Sequence 9, Appl	c 489	14	1.0	2360	2	US-08-039-384-1	Sequence 1, Appl
c 417	14	1.0	1512	1	US-07-853-985A-5	Sequence 5, Appl	c 490	14	1.0	2373	1	US-08-445-586-1	Sequence 1, Appl
c 418	14	1.0	1512	1	US-07-681-703B-5	Sequence 5, Appl	c 491	14	1.0	2382	1	US-08-256-938-1	Sequence 1, Appl
c 419	14	1.0	1512	1	US-08-184-236-5	Sequence 5, Appl	c 492	14	1.0	2384	1	US-07-814-964-10	Sequence 10, Appl
c 420	14	1.0	1512	3	US-08-407-410B-5	Sequence 5, Appl	c 493	14	1.0	2384	1	US-08-258-442-10	Sequence 10, Appl
c 421	14	1.0	1512	3	US-08-485-500-5	Sequence 5, Appl	c 494	14	1.0	2384	2	US-08-328-809-5	Sequence 5, Appl
c 422	14	1.0	1512	6	PCT-US91-02370-5	Sequence 5, Appl	c 495	14	1.0	2384	6	PCT-US92-11107-10	Sequence 10, Appl
c 423	14	1.0	1512	6	PCT-US94-0417A-5	Sequence 7, Appl	c 496	14	1.0	2387	1	US-08-288-408-4	Sequence 4, Appl
c 424	14	1.0	1523	1	US-08-184-327A-7	Sequence 7, Appl	c 497	14	1.0	2418	1	US-08-462-484-1	Sequence 1, Appl
c 425	14	1.0	1523	6	PCT-US95-00670-7	Sequence 7, Appl	c 498	14	1.0	2418	6	PCT-US95-07536-1	Sequence 1, Appl
c 426	14	1.0	1529	1	US-08-336-778-1	Sequence 1, Appl	c 499	14	1.0	2418	6	PCT-US95-07536-1	Sequence 1, Appl
c 427	14	1.0	1560	5	US-09-105-039A-1	Sequence 1, Appl	c 500	14	1.0	2454	1	US-08-359-696-3	Sequence 3, Appl
c 428	14	1.0	1561	3	US-08-532-547-2	Sequence 2, Appl	c 501	14	1.0	2455	1	US-08-256-938-3	Sequence 3, Appl
c 429	14	1.0	1561	3	US-08-379-656B-2	Sequence 2, Appl	c 502	14	1.0	2455	3	US-08-797-689-15	Sequence 15, Appl
c 430	14	1.0	1576	7	526043A-1	Patent No. 5260432	c 503	14	1.0	2503	5	US-08-691-563C-60	Sequence 60, Appl
c 431	14	1.0	1584	3	US-08-889-711-3	Sequence 3, Appl	c 504	14	1.0	2516	1	US-07-914-282D-2	Sequence 2, Appl
c 432	14	1.0	1596	3	US-08-807-861A-38	Sequence 38, Appl	c 505	14	1.0	2516	6	PCT-US93-02460-2	Sequence 2, Appl
c 433	14	1.0	1601	2	US-08-722-001-7	Sequence 7, Appl	c 506	14	1.0	2516	6	US-08-276-887A-2	Sequence 2, Appl
c 434	14	1.0	1605	5	US-09-105-039A-3	Sequence 3, Appl	c 507	14	1.0	2550	4	US-08-658-665-42	Sequence 42, Appl
c 435	14	1.0	1608	7	5221737-6	Patent No. 5221737	c 508	14	1.0	2550	4	US-08-658-665-44	Sequence 44, Appl
c 436	14	1.0	1633	1	US-08-197-792-42	Sequence 42, Appl	c 509	14	1.0	2571	1	US-07-171-331F-9	Sequence 9, Appl
c 437	14	1.0	1633	2	US-08-459-850-42	Sequence 42, Appl	c 510	14	1.0	2603	4	US-08-179-481-1	Sequence 1, Appl
c 438	14	1.0	1633	2	US-08-459-214-42	Sequence 42, Appl	c 511	14	1.0	2623	4	US-08-973-675-1	Sequence 1, Appl
c 439	14	1.0	1662	7	5198345-20	Patent No. 5198345	c 512	14	1.0	2631	1	US-08-208-036-13	Sequence 13, Appl
c 440	14	1.0	1689	1	US-08-442-884-2	Sequence 2, Appl	c 513	14	1.0	2631	2	US-08-428-823-13	Sequence 13, Appl
c 441	14	1.0	1757	1	US-08-313-075A-49	Sequence 49, Appl	c 514	14	1.0	2639	1	US-07-952-817-8	Sequence 8, Appl
c 442	14	1.0	1770	1	US-08-341-943-25	Sequence 25, Appl	c 515	14	1.0	2639	7	5210025-1	Patent No. 5210025
c 443	14	1.0	1779	1	US-08-208-036-16	Sequence 16, Appl	c 516	14	1.0	2655	4	US-08-868-786-3	Sequence 3, Appl
c 444	14	1.0	1779	2	US-08-428-823-16	Sequence 16, Appl	c 517	14	1.0	2656	4	US-08-685-625A-5	Sequence 5, Appl
c 445	14	1.0	1782	2	US-08-153-799-15	Sequence 15, Appl	c 518	14	1.0	2659	1	US-08-007-775-3	Sequence 3, Appl
c 446	14	1.0	1788	2	US-08-465-590-2	Sequence 2, Appl	c 519	14	1.0	2662	2	US-08-451-715A-5	Sequence 5, Appl
c 447	14	1.0	1788	4	US-08-722-806A-1	Sequence 1, Appl	c 520	14	1.0	2684	1	US-08-367-227-1	Sequence 1, Appl
c 448	14	1.0	1788	6	PCT-US93-08743-2	Sequence 2, Appl	c 521	14	1.0	2692	1	US-07-932-454A-2	Sequence 2, Appl
c 449	14	1.0	1813	6	PCT-US95-09345-1	Sequence 1, Appl	c 522	14	1.0	2716	1	US-08-647-484-1	Sequence 1, Appl
c 450	14	1.0	1813	3	US-08-007-107-1	Sequence 1, Appl	c 523	14	1.0	2716	1	US-08-647-484-3	Sequence 3, Appl
c 451	14	1.0	1827	4	US-08-824-878-2	Sequence 2, Appl	c 524	14	1.0	2716	1	US-08-647-481-1	Sequence 1, Appl
c 452	14	1.0	1830	1	US-07-691-079C-3	Sequence 3, Appl	c 525	14	1.0	2716	1	US-08-647-481-3	Sequence 3, Appl
c 453	14	1.0	1830	2	US-08-433-037-3	Sequence 3, Appl	c 526	14	1.0	2716	1	US-08-430-033A-1	Sequence 1, Appl
c 454	14	1.0	1830	4	US-08-702-572-1	Sequence 1, Appl	c 527	14	1.0	2716	1	US-08-430-033A-3	Sequence 3, Appl
c 455	14	1.0	1836	1	US-07-754-918A-1	Sequence 1, Appl	c 528	14	1.0	2716	6	PCT-US96-05792-1	Sequence 1, Appl
c 456	14	1.0	1851	6	PCT-US92-06969A-34	Sequence 34, Appl	c 529	14	1.0	2716	6	PCT-US96-05792-3	Sequence 3, Appl
c 457	14	1.0	1862	3	US-08-797-689-1	Sequence 1, Appl	c 530	14	1.0	2724	1	US-08-349-006-1	Sequence 1, Appl
c 458	14	1.0	1886	7	5210183-1	Patent No. 5210183	c 531	14	1.0	2724	4	US-08-658-665-37	Sequence 37, Appl
c 459	14	1.0	1929	4	US-08-818-253-1	Sequence 1, Appl	c 532	14	1.0	2724	6	PCT-US94-04180-1	Sequence 1, Appl
c 460	14	1.0	1929	4	US-08-818-253-5	Sequence 5, Appl	c 533	14	1.0	2745	2	US-08-363-255-1	Sequence 1, Appl
c 461	14	1.0	1944	7	5260223-2	Patent No. 5260223	c 534	14	1.0	2745	2	US-08-363-255-13	Sequence 13, Appl
c 462	14	1.0	1949	4	US-08-540-804-1	Sequence 1, Appl	c 535	14	1.0	2746	3	US-08-576-165-3	Sequence 3, Appl
c 463	14	1.0	1949	4	US-08-218-265-1	Sequence 1, Appl	c 536	14	1.0	2833	1	US-07-171-331F-1	Sequence 1, Appl
c 464	14	1.0	1959	4	US-08-818-253-3	Sequence 3, Appl	c 537	14	1.0	2877	4	US-08-317-401E-1	Sequence 1, Appl

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c 540	14	1.0	2911	3	US-08-588-983-11	Sequence 11, Appll	c 613	14	1.0	4200	1	US-07-841-654B-1	Sequence 1, Appll
c 541	14	1.0	2911	3	US-08-588-976-8	Sequence 8, Appll	c 614	14	1.0	4200	1	US-07-946-234A-1	Sequence 1, Appll
c 542	14	1.0	2911	3	US-08-588-976-11	Sequence 11, Appll	c 615	14	1.0	4200	1	US-08-123-161A-1	Sequence 1, Appll
c 543	14	1.0	2912	6	PCT-US91-01726-2	Sequence 2, Appll	c 616	14	1.0	4200	1	US-08-483-278-1	Sequence 1, Appll
c 544	14	1.0	2917	3	US-08-624-581-3	Sequence 3, Appll	c 617	14	1.0	4200	6	PCT-US93-01560-1	Sequence 1, Appll
c 545	14	1.0	2955	4	US-08-867-941-4	Sequence 4, Appll	c 618	14	1.0	4260	4	US-08-658-665-38	Sequence 38, Appll
c 546	14	1.0	2955	4	US-08-867-941-9	Sequence 9, Appll	c 619	14	1.0	4300	1	US-08-041-538-1	Sequence 1, Appll
c 547	14	1.0	2955	4	US-08-624-581-1	Sequence 1, Appll	c 620	14	1.0	4300	2	US-08-463-642-1	Sequence 1, Appll
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c 569	14	1.0	3484	1	US-08-530-492-105	Sequence 105, App	c 642	14	1.0	5399	2	US-08-368-071-9	Sequence 9, Appll
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c 580	14	1.0	3635	5	US-09-074-579-2	Sequence 2, Appll	c 653	14	1.0	5900	3	US-08-663-998-1	Sequence 1, Appll
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c 605	14	1.0	3934	3	US-08-779-046-3	Sequence 3, Appll	c 678	14	1.0	9401	3	US-08-432-693-1	Sequence 1, Appll
c 606	14	1.0	3934	4	US-08-881-340-3	Sequence 3, Appll	c 679	14	1.0	9401	6	PCT-US91-02225-9	Sequence 9, Appll
c 607	14	1.0	3957	1	US-07-689-008-5	Sequence 5, Appll	c 680	14	1.0	9540	1	US-07-689-008-1	Sequence 1, Appll
c 608	14	1.0	4000	3	US-08-861-464-5	Sequence 5, Appll	c 681	14	1.0	11663	1	US-08-446-932-1	Sequence 1, Appll
c 609	14	1.0	4000	4	US-08-396-001-5	Sequence 5, Appll	c 682	14	1.0	11663	2	US-08-801-263A-1	Sequence 1, Appll
c 610	14	1.0	4000	4	US-08-687-289A-2	Sequence 2, Appll	c 683	14	1.0	11663	2	US-08-801-263A-7	Sequence 7, Appll

C 684	14	1.0	11663	5	US-09-102-248-1	Sequence 1, Appl	C 757	13	0.9	36	3	US-08-585-584B-2033	Sequence 2033, Ap
C 685	14	1.0	11663	5	US-09-102-248-7	Sequence 7, Appl	C 758	13	0.9	36	3	US-08-585-584B-2034	Sequence 2034, Ap
C 686	14	1.0	11703	2	US-08-801-263A-8	Sequence 8, Appl	C 759	13	0.9	36	3	US-08-585-584B-2035	Sequence 2035, Ap
C 687	14	1.0	11703	5	US-09-102-248-8	Sequence 8, Appl	C 760	13	0.9	39	2	US-08-338-992B-3	Sequence 3, Appl
C 688	14	1.0	11717	2	US-08-801-263A-4	Sequence 4, Appl	C 761	13	0.9	39	2	US-08-338-992B-4	Sequence 4, Appl
C 689	14	1.0	11717	5	US-09-102-248-4	Sequence 4, Appl	C 762	13	0.9	39	2	US-08-750-810-3	Sequence 3, Appl
C 690	14	1.0	12001	4	US-08-458-568A-11	Sequence 11, Appl	C 763	13	0.9	39	3	US-08-750-810-4	Sequence 4, Appl
C 691	14	1.0	12225	4	US-08-822-445-11	Sequence 11, Appl	C 764	13	0.9	39	6	PCT-US95-09057-3	Sequence 3, Appl
C 692	14	1.0	12284	4	US-08-876-991-1	Sequence 1, Appl	C 765	13	0.9	39	6	PCT-US95-09057-4	Sequence 4, Appl
C 693	14	1.0	12284	4	US-09-059-853-1	Sequence 1, Appl	C 766	13	0.9	39	6	PCT-US95-09057-5	Sequence 5, Appl
C 694	14	1.0	12412	2	US-08-390-878-18	Sequence 18, Appl	C 767	13	0.9	50	4	US-08-525-058A-19	Sequence 19, Appl
C 695	14	1.0	12588	4	US-08-387-942C-1	Sequence 1, Appl	C 768	13	0.9	54	1	US-08-299-074A-19	Sequence 19, Appl
C 696	14	1.0	12616	4	US-08-822-445-9	Sequence 9, Appl	C 769	13	0.9	54	1	US-08-260-515-1	Sequence 1, Appl
C 697	14	1.0	12847	2	US-08-550-715-1	Sequence 1, Appl	C 770	13	0.9	54	4	US-08-622-556-1	Sequence 1, Appl
C 698	14	1.0	13254	1	US-08-276-852-156	Sequence 156, App	C 771	13	0.9	54	4	US-08-923-274-5	Sequence 5, Appl
C 699	14	1.0	13254	1	US-08-276-852-170	Sequence 170, App	C 772	13	0.9	54	4	US-08-959-536-5	Sequence 5, Appl
C 700	14	1.0	13254	2	US-08-899-575-156	Sequence 156, App	C 773	13	0.9	59	1	US-07-972-032-26	Sequence 26, Appl
C 701	14	1.0	13254	2	US-08-899-575-170	Sequence 170, App	C 774	13	0.9	59	1	US-07-972-032-27	Sequence 27, Appl
C 702	14	1.0	13254	2	US-08-899-575-156	Sequence 156, App	C 775	13	0.9	59	2	US-08-642-255-40	Sequence 40, Appl
C 703	14	1.0	13254	2	US-08-899-575-170	Sequence 170, App	C 776	13	0.9	59	2	US-08-642-255-41	Sequence 41, Appl
C 704	14	1.0	13254	6	PCT-US95-08743-156	Sequence 156, App	C 777	13	0.9	60	1	US-08-247-475-9	Sequence 9, Appl
C 705	14	1.0	13254	6	PCT-US95-08743-170	Sequence 170, App	C 778	13	0.9	60	1	US-08-479-650-9	Sequence 9, Appl
C 706	14	1.0	13473	6	PCT-US96-03916-1	Sequence 1, Appl	C 779	13	0.9	60	1	US-08-278-630A-1	Sequence 1, Appl
C 707	14	1.0	15239	2	US-08-390-878-17	Sequence 17, Appl	C 780	13	0.9	60	1	US-08-331-394-57	Sequence 57, Appl
C 708	14	1.0	16656	2	US-08-741-881-1	Sequence 1, Appl	C 781	13	0.9	60	2	US-08-250-858-57	Sequence 57, Appl
C 709	14	1.0	16656	3	US-08-739-158-1	Sequence 1, Appl	C 782	13	0.9	60	2	US-08-446-915-57	Sequence 57, Appl
C 710	14	1.0	16656	3	US-08-739-167-1	Sequence 1, Appl	C 783	13	0.9	60	2	US-08-191-8660-10	Sequence 10, Appl
C 711	14	1.0	18318	2	US-08-414-926A-6	Sequence 6, Appl	C 784	13	0.9	60	2	US-08-674-169-9	Sequence 9, Appl
C 712	14	1.0	18318	4	US-08-926-922-6	Sequence 6, Appl	C 785	13	0.9	60	3	US-08-744-139-55	Sequence 55, Appl
C 713	14	1.0	18912	6	PCT-US96-03916-59	Sequence 59, Appl	C 786	13	0.9	60	3	US-08-185-949B-10	Sequence 10, Appl
C 714	14	1.0	19011	1	US-08-310-356-36	Sequence 36, Appl	C 787	13	0.9	66	6	PCT-US95-06639-57	Sequence 57, Appl
C 715	14	1.0	19557	6	PCT-US92-06300-1	Sequence 1, Appl	C 788	13	0.9	66	2	US-08-323-531-23	Sequence 23, Appl
C 716	14	1.0	21126	1	US-08-008-218-19	Sequence 19, Appl	C 789	13	0.9	66	2	US-08-198-094-23	Sequence 23, Appl
C 717	14	1.0	21126	1	US-08-459-569-19	Sequence 19, Appl	C 790	13	0.9	66	2	US-08-606-789-28	Sequence 28, Appl
C 718	14	1.0	21126	2	US-08-458-831-19	Sequence 19, Appl	C 791	13	0.9	66	4	US-09-111-348-28	Sequence 28, Appl
C 719	14	1.0	28804	3	US-08-592-874-1	Sequence 1, Appl	C 792	13	0.9	66	6	PCT-US93-07424-23	Sequence 23, Appl
C 720	14	1.0	35100	3	US-08-770-379-18	Sequence 18, Appl	C 793	13	0.9	66	6	PCT-US95-02087-23	Sequence 23, Appl
C 721	14	1.0	43280	3	US-08-804-227C-1	Sequence 1, Appl	C 794	13	0.9	69	6	PCT-US95-04803-2	Sequence 2, Appl
C 722	14	1.0	55516	4	US-08-906-308-1	Sequence 1, Appl	C 795	13	0.9	73	1	US-08-260-515-10	Sequence 10, Appl
C 723	14	1.0	246240	3	US-08-724-394A-20	Sequence 20, Appl	C 796	13	0.9	74	1	US-08-360-515-4	Sequence 4, Appl
C 724	14	1.0	246240	3	US-08-724-394A-21	Sequence 21, Appl	C 797	13	0.9	74	1	US-08-260-515-12	Sequence 12, Appl
C 725	14	1.0	246240	3	US-08-724-394A-22	Sequence 22, Appl	C 798	13	0.9	74	1	US-08-360-515-16	Sequence 16, Appl
C 726	13	0.9	14	6	PCT-US96-09383-15	Sequence 15, Appl	C 799	13	0.9	74	1	US-08-260-515-19	Sequence 19, Appl
C 727	13	0.9	17	3	US-08-282-197C-16	Sequence 16, Appl	C 800	13	0.9	75	1	US-08-360-515-6	Sequence 6, Appl
C 728	13	0.9	19	1	US-08-031-143B-58	Sequence 58, Appl	C 801	13	0.9	76	6	PCT-US91-02942-43	Sequence 43, Appl
C 729	13	0.9	19	6	PCT-US94-02891-58	Sequence 58, Appl	C 802	13	0.9	77	4	US-08-477-527A-241	Sequence 241, App
C 730	13	0.9	20	2	US-08-801-263A-11	Sequence 11, Appl	C 803	13	0.9	77	6	PCT-US96-09537-241	Sequence 241, App
C 731	13	0.9	21	1	US-09-102-248-11	Sequence 11, Appl	C 804	13	0.9	85	1	US-08-479-783A-30	Sequence 30, Appl
C 732	13	0.9	21	5	US-08-240-547-39	Sequence 39, Appl	C 805	13	0.9	85	1	US-08-479-725-30	Sequence 30, Appl
C 733	13	0.9	23	3	US-08-197-770-5	Sequence 5, Appl	C 806	13	0.9	85	6	US-08-618-693-30	Sequence 30, Appl
C 734	13	0.9	26	3	US-08-482-182-21	Sequence 21, Appl	C 807	13	0.9	85	6	PCT-US96-08014-119	Sequence 119, App
C 735	13	0.9	26	3	US-08-482-182-64	Sequence 64, Appl	C 808	13	0.9	95	6	PCT-US95-09334-7	Sequence 7, Appl
C 736	13	0.9	26	4	US-08-766-439-48	Sequence 48, Appl	C 809	13	0.9	106	1	US-08-413-118-110	Sequence 110, App
C 737	13	0.9	27	2	US-08-758-306-702	Sequence 702, App	C 810	13	0.9	108	2	US-07-972-032-30	Sequence 30, Appl
C 738	13	0.9	29	2	US-08-530-492-14	Sequence 14, Appl	C 811	13	0.9	108	2	US-08-642-255-44	Sequence 44, Appl
C 739	13	0.9	29	2	US-08-464-531-35	Sequence 35, Appl	C 812	13	0.9	112	1	US-08-642-255-44	Sequence 44, Appl
C 740	13	0.9	29	3	US-08-461-598-35	Sequence 35, Appl	C 813	13	0.9	121	1	US-08-413-118-109	Sequence 109, App
C 741	13	0.9	30	1	US-07-969-931-27	Sequence 27, Appl	C 814	13	0.9	126	1	US-08-248-848-37	Sequence 37, Appl
C 742	13	0.9	30	1	US-07-855-417A-27	Sequence 27, Appl	C 815	13	0.9	126	2	US-08-111-077-37	Sequence 37, Appl
C 743	13	0.9	31	4	US-08-415-593-18	Sequence 18, Appl	C 816	13	0.9	135	1	US-08-161-406-3	Sequence 3, Appl
C 744	13	0.9	32	1	US-07-951-715A-43	Sequence 43, Appl	C 817	13	0.9	162	1	US-07-972-032-34	Sequence 34, Appl
C 745	13	0.9	32	3	US-08-459-448A-43	Sequence 43, Appl	C 818	13	0.9	162	1	US-07-972-032-36	Sequence 36, Appl
C 746	13	0.9	33	3	US-08-331-398A-29	Sequence 29, Appl	C 819	13	0.9	163	7	5486462-4	Patent No. 5486462
C 747	13	0.9	33	1	US-08-434-503-51	Sequence 51, Appl	C 820	13	0.9	194	2	US-08-606-789-11	Sequence 11, Appl
C 748	13	0.9	33	4	US-08-225-224-46	Sequence 46, Appl	C 821	13	0.9	194	2	US-09-111-348-11	Sequence 11, Appl
C 749	13	0.9	33	4	US-08-331-397B-29	Sequence 29, Appl	C 822	13	0.9	199	6	US-08-330-108-4	Sequence 4, Appl
C 750	13	0.9	33	4	US-08-759-804A-29	Sequence 29, Appl	C 823	13	0.9	199	6	PCT-US92-10087-4	Sequence 4, Appl
C 751	13	0.9	33	5	US-08-722-258-46	Sequence 46, Appl	C 824	13	0.9	216	1	US-07-972-032-46	Sequence 46, Appl
C 752	13	0.9	33	6	PCT-US95-04468-46	Sequence 46, Appl	C 825	13	0.9	216	1	US-08-031-143B-75	Sequence 75, Appl
C 753	13	0.9	36	1	US-07-792-585B-4	Sequence 4, Appl	C 826	13	0.9	217	2	US-08-470-892-3	Sequence 3, Appl
C 754	13	0.9	36	1	US-08-423-398B-25	Sequence 25, Appl	C 827	13	0.9	219	1	US-07-989-363-3	Sequence 3, Appl
C 755	13	0.9	36	2	US-08-334-847-225	Sequence 225, App	C 828	13	0.9	219	1	US-08-264-526-3	Sequence 3, Appl
C 756	13	0.9	36	2	US-08-334-847-742	Sequence 742, App	C 829	13	0.9	240	2	US-08-485-455D-58	Sequence 58, Appl

830	13	0.9	240	4	US-08-484-211C-58	Sequence 58, Appl	c 903	13	0.9	489	1	US-08-081-072-9	Sequence 9, Appl
831	13	0.9	240	6	PCT-US95-1442A-58	Sequence 58, Appl	c 904	13	0.9	489	1	US-08-449-093A-9	Sequence 9, Appl
832	13	0.9	252	1	US-08-260-202A-26	Sequence 26, Appl	c 905	13	0.9	496	2	US-08-263-413-23	Sequence 23, Appl
833	13	0.9	263	2	US-08-594-031-108	Sequence 108, App	c 906	13	0.9	498	1	US-08-412-614-90	Sequence 90, Appl
834	13	0.9	265	2	US-08-709-616-2	Sequence 2, Appl	c 907	13	0.9	498	4	US-08-635-761-90	Sequence 22, Appl
835	13	0.9	276	1	US-07-800-370-1	Sequence 1, Appl	c 908	13	0.9	500	2	US-08-263-413-22	Sequence 17, Appl
836	13	0.9	276	1	US-08-057-168-1	Sequence 1, Appl	c 909	13	0.9	507	1	US-08-310-416A-17	Sequence 17, Appl
837	13	0.9	277	2	US-08-518-878B-18	Sequence 18, Appl	c 910	13	0.9	507	3	US-08-888-171-17	Sequence 1, Appl
838	13	0.9	277	2	US-08-518-878B-19	Sequence 19, Appl	c 911	13	0.9	514	3	US-08-705-625-1	Sequence 1, Appl
839	13	0.9	277	2	US-08-294-522B-18	Sequence 18, Appl	c 912	13	0.9	518	4	US-08-557-309B-1	Sequence 23, Appl
840	13	0.9	277	2	US-08-294-522B-19	Sequence 19, Appl	c 913	13	0.9	519	4	US-08-799-464A-23	Sequence 23, Appl
841	13	0.9	277	3	US-08-807-861A-18	Sequence 18, Appl	c 914	13	0.9	519	6	PCT-US95-09927-23	Sequence 23, Appl
842	13	0.9	277	3	US-08-807-861A-19	Sequence 19, Appl	c 915	13	0.9	522	6	US-08-131-625B-15	Sequence 15, Appl
843	13	0.9	277	3	US-08-470-868A-18	Sequence 18, Appl	c 916	13	0.9	522	6	PCT-US95-10904-23	Sequence 23, Appl
844	13	0.9	277	3	US-08-470-868A-19	Sequence 19, Appl	c 917	13	0.9	525	1	US-08-485-359-1	Sequence 1, Appl
845	13	0.9	292	2	US-08-606-789-14	Sequence 14, Appl	c 918	13	0.9	525	1	US-08-569-594-1	Sequence 1, Appl
846	13	0.9	292	4	US-09-111-348-14	Sequence 14, Appl	c 919	13	0.9	525	1	US-08-434-411-1	Sequence 1, Appl
847	13	0.9	302	1	US-08-189-139A-1	Sequence 1, Appl	c 920	13	0.9	525	2	US-08-434-402-1	Sequence 1, Appl
848	13	0.9	303	4	US-08-865-273-3	Sequence 3, Appl	c 921	13	0.9	525	2	US-08-783-288-1	Sequence 1, Appl
849	13	0.9	312	1	US-08-008-216-5	Sequence 5, Appl	c 922	13	0.9	525	4	US-08-890-640-1	Sequence 1, Appl
850	13	0.9	312	1	US-08-459-569-5	Sequence 5, Appl	c 923	13	0.9	525	6	PCT-US94-12873-1	Sequence 1, Appl
851	13	0.9	312	2	US-08-459-831-5	Sequence 5, Appl	c 924	13	0.9	525	6	PCT-US96-08815-1	Sequence 1, Appl
852	13	0.9	331	3	US-07-916-038A-22	Sequence 22, Appl	c 925	13	0.9	525	7	PCT-US96-08815-1	Sequence 1, Appl
853	13	0.9	333	4	US-08-958-201-13	Sequence 13, Appl	c 926	13	0.9	537	1	US-08-176-620A-9	Sequence 9, Appl
854	13	0.9	354	3	US-08-652-816A-23	Sequence 23, Appl	c 927	13	0.9	537	1	US-08-461-985-9	Sequence 9, Appl
855	13	0.9	357	7	5486462-8	Sequence 7, Appl	c 928	13	0.9	537	6	PCT-US94-12873-16	Sequence 16, Appl
856	13	0.9	363	2	US-08-594-031-104	Sequence 104, App	c 929	13	0.9	541	3	US-08-797-689-13	Sequence 13, Appl
857	13	0.9	363	3	US-07-916-038A-8	Sequence 8, Appl	c 930	13	0.9	545	2	US-08-599-252-86	Sequence 86, Appl
858	13	0.9	366	3	US-07-916-038A-9	Sequence 9, Appl	c 931	13	0.9	545	6	PCT-US95-06406A-22	Sequence 22, Appl
859	13	0.9	367	3	US-08-967-101-24	Sequence 24, Appl	c 932	13	0.9	545	6	PCT-US96-06352-86	Sequence 86, Appl
860	13	0.9	367	4	US-08-592-541-24	Sequence 24, Appl	c 933	13	0.9	545	6	PCT-US96-06583-86	Sequence 86, Appl
861	13	0.9	390	2	US-08-844-085-3	Sequence 3, Appl	c 934	13	0.9	546	6	PCT-US95-01185-177	Sequence 177, App
862	13	0.9	390	5	US-08-803-085-1	Sequence 1, Appl	c 935	13	0.9	546	6	PCT-US95-01185-178	Sequence 178, App
863	13	0.9	392	1	US-08-318-193-1	Sequence 1, Appl	c 936	13	0.9	546	6	PCT-US95-01185-179	Sequence 179, App
864	13	0.9	393	1	US-07-846-992-10	Sequence 10, Appl	c 937	13	0.9	549	1	US-08-412-614-92	Sequence 92, Appl
865	13	0.9	393	1	US-08-469-555-10	Sequence 10, Appl	c 938	13	0.9	549	4	US-08-635-761-92	Sequence 92, Appl
866	13	0.9	394	2	US-08-471-780C-103	Sequence 103, App	c 939	13	0.9	555	6	PCT-US94-12873-13	Sequence 13, Appl
867	13	0.9	394	2	US-08-471-780C-103	Sequence 103, App	c 940	13	0.9	555	6	PCT-US94-12873-13	Sequence 13, Appl
868	13	0.9	394	3	US-08-471-282A-103	Sequence 103, App	c 941	13	0.9	560	3	US-08-484-993B-44	Sequence 44, Appl
869	13	0.9	394	3	US-08-466-710C-103	Sequence 103, App	c 942	13	0.9	560	4	US-08-484-158B-44	Sequence 44, Appl
870	13	0.9	396	1	US-08-470-179-58	Sequence 58, Appl	c 943	13	0.9	560	4	US-08-484-996A-44	Sequence 44, Appl
871	13	0.9	406	1	US-08-318-193-52	Sequence 52, Appl	c 944	13	0.9	560	5	US-08-480-150A-44	Sequence 44, Appl
872	13	0.9	414	4	US-09-067-773-6	Sequence 2, Appl	c 945	13	0.9	561	6	PCT-US95-04971-13	Sequence 13, Appl
873	13	0.9	414	4	US-09-067-773-6	Sequence 6, Appl	c 946	13	0.9	561	6	US-08-463-115-32	Sequence 32, Appl
874	13	0.9	414	4	US-09-067-773-9	Sequence 9, Appl	c 947	13	0.9	563	2	US-08-463-388-32	Sequence 32, Appl
875	13	0.9	420	3	US-08-736-334B-33	Sequence 33, Appl	c 948	13	0.9	574	6	PCT-US95-06994-2	Sequence 2, Appl
876	13	0.9	422	1	US-07-920-519-33	Sequence 33, Appl	c 949	13	0.9	581	3	US-08-505-617-5	Sequence 5, Appl
877	13	0.9	422	1	US-08-314-586-33	Sequence 33, Appl	c 950	13	0.9	581	4	US-09-018-170-5	Sequence 5, Appl
878	13	0.9	422	1	US-08-470-179-73	Sequence 73, Appl	c 951	13	0.9	585	2	US-08-420-235B-8	Sequence 8, Appl
879	13	0.9	422	1	US-08-371-121-13	Sequence 13, Appl	c 952	13	0.9	585	6	PCT-US95-10194-8	Sequence 8, Appl
880	13	0.9	422	5	US-07-927-391-14	Sequence 14, Appl	c 953	13	0.9	586	2	US-07-869-933-26	Sequence 26, Appl
881	13	0.9	423	1	US-08-470-179-67	Sequence 67, Appl	c 954	13	0.9	595	1	US-08-260-202A-1	Sequence 1, Appl
882	13	0.9	423	1	US-08-470-179-72	Sequence 72, Appl	c 955	13	0.9	595	1	US-08-017-114-1	Sequence 1, Appl
883	13	0.9	423	1	US-08-470-179-81	Sequence 81, Appl	c 956	13	0.9	595	6	PCT-US94-02034-1	Sequence 1, Appl
884	13	0.9	423	1	US-08-470-179-83	Sequence 83, Appl	c 957	13	0.9	596	3	US-08-676-279-63	Sequence 63, Appl
885	13	0.9	423	1	US-08-470-179-85	Sequence 85, Appl	c 958	13	0.9	597	2	US-08-406-248-3	Sequence 3, Appl
886	13	0.9	423	1	US-08-470-179-96	Sequence 96, Appl	c 959	13	0.9	599	4	US-08-809-297-43	Sequence 43, Appl
887	13	0.9	423	1	US-08-470-179-96	Sequence 130, App	c 960	13	0.9	600	2	US-08-602-262-4	Sequence 4, Appl
888	13	0.9	423	1	US-08-470-179-168	Sequence 168, App	c 961	13	0.9	600	2	US-08-602-262-5	Sequence 5, Appl
889	13	0.9	423	1	US-08-470-179-169	Sequence 169, App	c 962	13	0.9	600	2	US-08-602-262-5	Sequence 5, Appl
890	13	0.9	423	1	US-08-470-179-190	Sequence 190, App	c 963	13	0.9	616	2	US-08-463-115-13	Sequence 13, Appl
891	13	0.9	423	1	US-08-470-179-191	Sequence 191, App	c 964	13	0.9	616	2	US-08-465-388-13	Sequence 13, Appl
892	13	0.9	423	1	US-08-470-179-194	Sequence 194, App	c 965	13	0.9	629	4	US-08-809-297-44	Sequence 44, Appl
893	13	0.9	432	2	US-08-642-255-48	Sequence 48, App	c 966	13	0.9	630	1	US-08-185-414E-1	Sequence 1, Appl
894	13	0.9	447	4	US-08-387-942C-33	Sequence 33, Appl	c 967	13	0.9	633	2	US-08-644-664B-6	Sequence 6, Appl
895	13	0.9	447	4	US-08-387-942C-33	Sequence 33, Appl	c 968	13	0.9	633	4	US-08-761-277-6	Sequence 6, Appl
896	13	0.9	450	2	US-08-399-580B-2	Sequence 2, Appl	c 969	13	0.9	636	3	US-08-284-941-3	Sequence 3, Appl
897	13	0.9	453	2	US-08-470-892-4	Sequence 4, Appl	c 970	13	0.9	636	6	PCT-US93-02147A-3	Sequence 3, Appl
898	13	0.9	454	4	US-08-680-326-118	Sequence 118, App	c 971	13	0.9	641	1	US-07-846-992-9	Sequence 9, Appl
899	13	0.9	461	3	US-07-916-098A-38	Sequence 38, Appl	c 972	13	0.9	641	1	US-08-469-555-9	Sequence 9, Appl
900	13	0.9	487	1	US-08-485-359-3	Sequence 3, Appl	c 973	13	0.9	642	1	US-08-287-442-1	Sequence 1, Appl
901	13	0.9	487	1	US-08-569-594-3	Sequence 3, Appl	c 974	13	0.9	642	1	US-08-287-442-1	Sequence 1, Appl
902	13	0.9	487	6	PCT-US96-08815-3	Sequence 3, Appl	c 975	13	0.9	642	1	US-08-287-442-5	Sequence 5, Appl

976 13 0.9 642 1 US-08-459-701-1
977 13 0.9 642 1 US-08-459-701-5
978 13 0.9 642 1 US-08-460-298-1
979 13 0.9 642 1 US-08-460-298-5
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981 13 0.9 642 2 US-08-459-174-5
982 13 0.9 642 2 US-08-761-258-2
983 13 0.9 642 2 US-08-761-258-4
984 13 0.9 642 2 US-08-761-258-9
985 13 0.9 642 3 US-09-009-218-1
986 13 0.9 642 3 US-09-009-218-3
987 13 0.9 642 3 US-09-009-218-5
988 13 0.9 642 3 US-09-009-218-7
989 13 0.9 642 3 US-09-009-218-9
990 13 0.9 642 4 US-08-977-306-2
991 13 0.9 642 4 US-08-977-306-4
992 13 0.9 642 4 US-08-977-306-9
993 13 0.9 642 6 PCT-US93-06300A-1
994 13 0.9 642 6 PCT-US93-06300A-5
c 995 13 0.9 657 1 US-08-412-108-2
996 13 0.9 653 2 US-08-506-404B-1
c 997 13 0.9 664 3 US-08-835-099A-15
c 998 13 0.9 675 1 US-07-807-043B-2
c 999 13 0.9 675 1 US-08-299-849B-2
c1000 13 0.9 675 4 US-08-142-368A-2

ALIGNMENTS

RESULT 1
US-08-764-233A-1/c
; Sequence 1, Application US/08764233A
; Patent No. 5716849
; GENERAL INFORMATION:
; APPLICANT: Ligon, James M.
; APPLICANT: Schupp, Thomas
; APPLICANT: Beck, James J.
; APPLICANT: Hill, Dwight S.
; APPLICANT: Neff, Snezhana
; APPLICANT: Ryals, John A.
; TITLE OF INVENTION: Genes For The Biosynthesis Of Soraphen
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/764,233A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/729,214
; FILING DATE: 09-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/258,261
; FILING DATE: 08-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: 1506/CIP6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
; LENGTH: 49377 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Sorangium cellulosum
; IMMEDIATE SOURCE:
; CLONE: p98/1, pJL3, and pVKM15
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 383..760
; OTHER INFORMATION: /product= "SorB"
; OTHER INFORMATION: /note= "This gene encodes a protein that is highly homolog
; OTHER INFORMATION: the reductase domains of type I PKs such as eryA from
; OTHER INFORMATION: Saccharopolyspora erythraea."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 927..19874
; OTHER INFORMATION: /product= "SorA"
; OTHER INFORMATION: /note= "Gene product is highly homologous to type I PKs
; OTHER INFORMATION: are known to be involved in the synthesis of polyketide
; OTHER INFORMATION: compounds."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 942..7115
; OTHER INFORMATION: /product= "Module 1 of SorA"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 7203..12884
; OTHER INFORMATION: /product= "Module 2 of SorA"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 13455..19616
; OTHER INFORMATION: /product= "Module 3 of SorA"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 19871..46318
; OTHER INFORMATION: /product= "SorB"
; OTHER INFORMATION: /note= "Gene product is highly homologous to type I PKs ge
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 19870..24556
; OTHER INFORMATION: /product= "Module 1 of SorB"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 24638..30820
; OTHER INFORMATION: /product= "Module 2 of SorB"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 30881..35446
; OTHER INFORMATION: /product= "Module 3 of SorB"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 35528..40114
; OTHER INFORMATION: /product= "Module 4 of SorB"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 40190..46318
; OTHER INFORMATION: /product= "Module 5 of SorB"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 46851..47891
; OTHER INFORMATION: /product= "SorM"
; OTHER INFORMATION: /note= "The protein encoded by the sorM gene is highly
; OTHER INFORMATION: homologous to the methyltransferase from Streptomyces
; OTHER INFORMATION: hygroscopicus that is involved in the synthesis of the
; OTHER INFORMATION: polyketide rapamycin."
; US-08-764-233A-1

Query Match

1.2%; Score 17; DB 2; Length 49377;

Best Local Similarity 100.0%; Pred. No. 19;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 401 acggctacatcctgacc 417
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Db 49054 ACGGCTACATCCTGACC 49038

RESULT 2
PCT-US91-02942-27/c
; Sequence 27, Application PC/TUS9102942
; GENERAL INFORMATION:
; APPLICANT: ROTHLEIN, ROBERT
; APPLICANT: ADAIR, JOHN R
; APPLICANT: ATHWAL, DILJEET S
; TITLE OF INVENTION: HUMANIZED CDR-GRAFTED ICAM-1 ANTIBODY
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1225 Connecticut Ave. NW Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/02942
; FILING DATE: 19910429
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9009549.8
; FILING DATE: 27-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: FOX, SAM L
; REGISTRATION NUMBER: 30,353
; REFERENCE/DOCKET NUMBER: 1011.0586600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 466-0800
; TELEFAX: (202) 833-8716
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 76 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US91-02942-27

Query Match 1.1%; Score 16; DB 6; Length 76;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1348 ttaaggcagcgagc 1363
|||||
Db 32 TTAAGGCAGCGGACG 17

RESULT 3
US-08-171-385-10/c
; Sequence 10, Application US/08171385
; Patent No. 5527884
; GENERAL INFORMATION:
; APPLICANT: Mary E. Russell
; APPLICANT: Ulrike Utans
; TITLE OF INVENTION: Mediators of Chronic Allograft
; TITLE OF INVENTION: Rejection
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55Sx
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/171,385
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 05433/006001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 388
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-171-385-10

Query Match 1.1%; Score 16; DB 1; Length 388;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 344 aagaagaagcagatga 359
|||||
Db 305 AAGAAGAAGCAGATGA 290

RESULT 4
US-08-534-910B-4/c
; Sequence 4, Application US/08534910B
; Patent No. 5766911
; GENERAL INFORMATION:
; APPLICANT: KOIKE, Ayumi
; APPLICANT: OBATA, Shusei
; APPLICANT: NISHINO, Tokuzo
; APPLICANT: OHNUMA, Shinichi
; APPLICANT: NAKAZAWA, Takeshi
; APPLICANT: OGURA, Kyoza
; APPLICANT: KOYAMA, Tanetoshi
; TITLE OF INVENTION: Mutated Farnesylidiphosphate Synthase Capable
; TITLE OF INVENTION: Of Synthesizing Geranylgeranyldiphosphate And Gene Coding
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: 1025 Connecticut Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.
; ZIP: 20036-5405
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.25" Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
; SOFTWARE: IBM/Word Perfect 6.1 Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/534,910B

;
; FILING DATE: 28-SEPT-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-25253
; FILING DATE: 14-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Toffenetti, Judith L.
; REGISTRATION NUMBER: 39,048
; REFERENCE/DOCKET NUMBER: 77670/398
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)429-1776
; TELEFAX: (202)429-0796
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 894 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; ORIGINAL SOURCE:
; ORGANISM: Bacillus stearothermophilus
; US-08-534-910B-4

Query Match 1.1%; Score 16; DB 2; Length 894;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 269 ccgaccgcgttgccga 284
|||||
DB 722 CCGACCGCGTTCGCA 707

RESULT 5
US-08-860-368B-4
; Sequence 4, Application US/08860368B
; Patent No. 6002072
; GENERAL INFORMATION:
; APPLICANT: McMaster, Russell J.
; APPLICANT: Boeshore, Maury L.
; APPLICANT: Tricoli, David M.
; APPLICANT: Reynolds, John F.
; APPLICANT: Carney, Kim J.
; APPLICANT: Gonsalves, Dennis
; TITLE OF INVENTION: Papaya Ringspot Virus Coat Protein Gene
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
; STREET: 180 N. Stetson Avenue, 2 Prudential Plaza,
; CITY: Suite 4700
; STATE: IL
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa L.
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0181US
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5400
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 929 base pairs

;
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3..872
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 876..929
; US-08-860-368B-4

Query Match 1.1%; Score 16; DB 5; Length 929;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 139 gacgcagctgtcagta 154
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DB 780 GACGCAGTGTCA GTA 795

RESULT 6
US-08-860-368B-19
; Sequence 19, Application US/08860368B
; Patent No. 6002072
; GENERAL INFORMATION:
; APPLICANT: McMaster, Russell J.
; APPLICANT: Boeshore, Maury L.
; APPLICANT: Tricoli, David M.
; APPLICANT: Reynolds, John F.
; APPLICANT: Carney, Kim J.
; APPLICANT: Gonsalves, Dennis
; TITLE OF INVENTION: Papaya Ringspot Virus Coat Protein Gene
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
; STREET: 180 N. Stetson Avenue, 2 Prudential Plaza,
; CITY: Suite 4700
; STATE: IL
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa L.
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0181US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5400
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1155 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: DNA (genomic)
; US-08-860-368B-19

Query Match 1.1%; Score 16; DB 5; Length 1155;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,008
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,063
FILING DATE: 13-SEP-1994
APPLICATION NUMBER: US 07/749,611
FILING DATE: 28-AUG-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/576,537
FILING DATE: 31-AUG-1990
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10660)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 1479 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 107..1438
US-08-476-008-68

Query Match 1.1%; Score 16; DB 1; Length 1479;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 481 accgccaaactcatcg 496
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DB 1299 ACCGCCAAACTCATCG 1284

RESULT 10
US-08-306-063-68/c
Sequence 68, Application US/08306063
Patent No. 5633435
GENERAL INFORMATION:
APPLICANT: Barry, Gerard F.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Padgett, Stephen R.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,063
FILING DATE: 13-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,611
FILING DATE: 28-AUG-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/576,537
FILING DATE: 31-AUG-1990
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10660)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 1479 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 107..1438
US-08-306-063-68

Query Match 1.1%; Score 16; DB 1; Length 1479;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 481 accgccaaactcatcg 496
|||||
DB 1299 ACCGCCAAACTCATCG 1284

RESULT 11
US-08-833-485-68/c
Sequence 68, Application US/08833485
Patent No. 5804425
GENERAL INFORMATION:
APPLICANT: Barry, Gerard F.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Padgett, Stephen R.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,485
FILING DATE: 07-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,063
FILING DATE: 13-SEP-1994
CLASSIFICATION: 435

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,611
; FILING DATE: 28-AUG-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: US 07/576,537
; APPLICATION NUMBER: 31-AUG-1990
; FILING DATE: 31-AUG-1990
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner Jr., Dennis R.
; REGISTRATION NUMBER: 30,914
; REFERENCE/DOCKET NUMBER: 38-21(15117)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)737-6099
; TELEFAX: (314)737-6047
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1479 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 107..1438
; US-08-833-485-68

Query Match 1.1%; Score 16; DB 2; Length 1479;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 481 accgccaactcatcg 496
|||||
DB 1299 ACCGCCAACTCATCG 1284

RESULT 12
US-08-204-656B-9
; Sequence 9, Application US/08204656B
; Patent No. 5538882
; GENERAL INFORMATION:
; APPLICANT: Matsui, Ikuo
; APPLICANT: Ishikawa, Kazuhiko
; APPLICANT: Miyairi, Sachio
; APPLICANT: Honda, Koichi
; TITLE OF INVENTION: Variant-Type Carbohydrate Hydrolase,
; TITLE OF INVENTION: Variant Gene Of The Enzyme And Method For Producing
; TITLE OF INVENTION: Oligosaccharide Using The Enzyme
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/204,656B
; FILING DATE: 02-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiner, Marc S.
; REGISTRATION NUMBER: 32,181
; REFERENCE/DOCKET NUMBER: 234-252P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050

```

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; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2061 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic DNA"
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; LIBRARY: Library of chromosomal DNA from Bacillus
; LIBRARY: macerans, pMAC, generated by treating chromosomal DNA from Bacillus
; LIBRARY: IAM1243 with a restriction enzyme, and inserting and linking restric
; LIBRARY: fragments to pBR322
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2061
; OTHER INFORMATION: /note= "Nucleotides 1-2061
; OTHER INFORMATION: correspond to nucleotides 82-2142 of the Bacillus macerans
; OTHER INFORMATION: cyclomaltodextrin glucanotransferase structural gene"
; US-08-204-656B-9

Query Match 1.1%; Score 16; DB 1; Length 2061;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1171 ggcaacgccgcgcgac 1186
|||||
DB 1825 GGCAACGCCGCCGAGC 1840

RESULT 13
US-08-470-702-5
; Sequence 5, Application US/08470702
; Patent No. 5631149
; GENERAL INFORMATION:
; APPLICANT: MATSUI, IKUO
; APPLICANT: ISHIKAWA, KAZUHIKO
; APPLICANT: MIYAIRI, SACHIO
; APPLICANT: HONDA, KOICHI
; TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE HYDROLASE.
; TITLE OF INVENTION: VARIANT GENE OF THE ENZYME AND METHOD FOR PRODUCING
; TITLE OF INVENTION: OLIGOSACCHARIDE USING THE ENZYME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,702
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/204,656
; FILING DATE: 02-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: WEINER, MARC S.
; REGISTRATION NUMBER: 32,181
; REFERENCE/DOCKET NUMBER: 234-252P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050

```

TELEX: 248345
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2061 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (synthetic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-470-702-5

Query Match 1.1%; Score 16; DB 1; Length 2061;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1171 ggcaacgcgcgcgacg 1186
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Db 1825 ggcaacgcgcgcgacg 1840

RESULT 14

US-08-467-831-5
Sequence 5, Application US/08467831
Patent No. 5635378
GENERAL INFORMATION:
APPLICANT: MATSUI, IKUO
APPLICANT: ISHIKAWA, KAZUHIKO
APPLICANT: MIYAIRI, SACHIO
APPLICANT: HONDA, KOICHI
TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE HYDROLASE,
TITLE OF INVENTION: VARIANT GENE OF THE ENZYME AND METHOD FOR PRODUCING
TITLE OF INVENTION: OLIGOSACCHARIDE USING THE ENZYME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 Gatehouse Road, Suite 500 East
CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22042

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,831
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/204,656
FILING DATE: 02-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 234-252P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
TELEX: 248345

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2061 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (synthetic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-467-831-5

Query Match 1.1%; Score 16; DB 1; Length 2061;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1171 ggcaacgcgcgcgacg 1186
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Db 1825 ggcaacgcgcgcgacg 1840

RESULT 15

US-08-132-990A-7
Sequence 7, Application US/08132990A
Patent No. 5834589
GENERAL INFORMATION:
APPLICANT: MERUELO, DANIEL
APPLICANT: YOSHIMOTO, TAKAYUKI
TITLE OF INVENTION: Human Retrovirus Receptor and DNA Coding Therefor
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/132,990A
FILING DATE: 07-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/084,729
FILING DATE: 29-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05569
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/899,075
FILING DATE: 11-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/806,178
FILING DATE: 13-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/627,950
FILING DATE: 14-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 8105-004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66441 PENNIE
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2157 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 148..2034
US-08-132-990A-7

Query Match 1.1%; Score 16; DB 3; Length 2157;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

us-09-388-090-3.oligo.rni

Tue Apr 18 14:24:58 2000

Qy 450 caaagtcctgctcaac 465
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Db 156 CAAAGTCCTGCTCAAC 171

Search completed: April 14, 2000, 18:27:45
Job time: 7077 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2000, 17:42:31 ; Search time 1303.77 Seconds
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Title: US-09-388-090-3
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Gapop 60.0 , Gapext 60.0

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Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	20	1.4	458	27	AA013893	AA013893 m04b12.r	c 78	17	1.2	322	33	AA362064	AA362064 EST71717
6	20	1.4	462	33	AA447906	AA447906 x211b06.f	c 79	17	1.2	326	25	N77431	N77431 y*31908.r1
7	20	1.4	481	44	AI322461	AI322461 m04b12.y	c 80	17	1.2	328	50	AI674135	AI674135 wd08b02.x
8	19	1.4	557	44	AI322461	AI322461 m04b12.y	c 81	17	1.2	328	64	AW016622	AW016622 UI-H-B10p
9	19	1.4	354	37	AA672965	AA672965 v048b11.i	c 82	17	1.2	329	31	AAW050788	AAW050788 w221e04.x
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22	18	1.3	488	91	AQ316002	AQ316002 HS_3055_B	c 95	17	1.2	360	28	CI3485	CI3485 C13485 YUJ1
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24	18	1.3	551	21	T62818	T62818 yc70b04.s1	c 97	17	1.2	360	36	C65143	C65143 C65143 YUJ1
25	18	1.3	564	63	AI947590	AI947590 603024D11	c 98	17	1.2	360	62	AV186467	AV186467 AV186467
26	18	1.3	597	100	AQ276833	AQ276833 CITBI-E1-	c 99	17	1.2	360	62	AV192074	AV192074 AV192074
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29	18	1.3	668	104	AQ543740	AQ543740 GPC1-11-3	c 102	17	1.2	363	44	AI277668	AI277668 ql78f03.x
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31	18	1.3	723	91	AQ158994	AQ158994 nbxb0012L	c 104	17	1.2	370	73	AW170669	AW170669 x185g05.x
32	18	1.3	756	34	AA519798	AA519798 TGESTgz35	c 105	17	1.2	376	104	AQ513981	AQ513981 HS_5179_B
33	18	1.3	756	91	AQ163302	AQ163302 mgxb0023P	c 106	17	1.2	379	31	AA326832	AA326832 EST30067
34	18	1.3	806	45	AI356845	AI356845 qy16d12.x	c 107	17	1.2	379	49	AI628510	AI628510 ty94h01.x
35	18	1.3	893	80	AF075974	AF075974 Salmonell	c 108	17	1.2	384	30	AA225545	AA225545 nc0bb08.s
36	18	1.3	901	80	AF075966	AF075966 Salmonell	c 109	17	1.2	391	63	AI933675	AI933675 nc42a10.x
37	18	1.3	973	80	AF075860	AF075860 Salmonell	c 110	17	1.2	392	100	AQ262683	AQ262683 CITBI-E1-
38	18	1.3	977	80	AF075892	AF075892 Salmonell	c 111	17	1.2	393	45	AI356408	AI356408 qz28g10.x
39	18	1.3	1050	79	CNS000GRM	AL072458 Drosophill	c 112	17	1.2	393	63	AI980829	AI980829 pat.pK003
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42	18	1.3	1101	79	CNS00120	AL056113 Drosophill	c 115	17	1.2	398	36	AA645936	AA645936 vn11d12.r
43	17	1.2	73	40	AA931149	AA931149 o070c09.s	c 116	17	1.2	398	44	AI261749	AI261749 qk10a03.x
44	17	1.2	106	27	AA024642	AA024642 z679a05.r	c 117	17	1.2	401	24	N25993	N25993 yx88d06.s1
45	17	1.2	117	42	AI126325	AI126325 q082f03.x	c 118	17	1.2	402	34	AA485476	AA485476 ab09b06.r
46	17	1.2	124	45	AI355872	AI355872 q002f10.x	c 119	17	1.2	402	37	T45453	T45453 8716 Lambda
47	17	1.2	127	90	AQ025988	AQ025988 EP(2)0380	c 120	17	1.2	403	20	246535	246535 ATTS4279 Ve
48	17	1.2	135	64	AW073768	AW073768 x012g08.x	c 121	17	1.2	403	22	R75793	R75793 Y121f09.r1
49	17	1.2	133	47	AI496080	AI496080 sa95f03.y	c 122	17	1.2	403	64	AW016764	AW016764 UI-H-B10p
50	17	1.2	145	26	W85266	W85266 mf45h12.r1	c 123	17	1.2	403	64	AW028747	AW028747 wv34e01.x
51	17	1.2	148	60	AI794914	AI794914 s073601.y	c 124	17	1.2	403	74	AW206271	AW206271 UI-H-B11-
52	17	1.2	151	74	AW225218	AW225218 687054C04	c 125	17	1.2	405	25	N75881	N75881 yw32f04.r1
53	17	1.2	193	20	D12142	D12142 HUM0005240	c 126	17	1.2	406	43	AI244839	AI244839 qj98d09.x
54	17	1.2	193	62	AI905624	AI905624 CM-BT094-	c 127	17	1.2	408	74	AW220812	AW220812 EST297281
55	17	1.2	211	63	AW009718	AW009718 ws8e10.x	c 128	17	1.2	409	46	AI454973	AI454973 LD01523.5
56	17	1.2	224	62	AI905837	AI905837 IL-BT099-	c 129	17	1.2	410	45	AI418060	AI418060 tf73f02.x
57	17	1.2	258	46	AI441034	AI441034 sa58e08.y	c 130	17	1.2	411	22	R36898	R36898 yf52h07.s1
58	17	1.2	286	31	AA302590	AA302590 EST15812	c 131	17	1.2	411	51	AI717148	AI717148 UI-R-Y0-a
59	17	1.2	289	61	AI833248	AI833248 at76e07.x	c 132	17	1.2	413	42	AI124048	AI124048 qa94h04.s
60	17	1.2	290	32	AA341610	AA341610 EST47198	c 133	17	1.2	413	49	AI636198	AI636198 tz06f08.x
61	17	1.2	294	32	AA340069	AA340069 EST45219	c 134	17	1.2	414	40	AA909176	AA909176 o112a05.s
62	17	1.2	295	70	AV224407	AV224407 AV224407	c 135	17	1.2	414	40	AA921758	AA921758 om43g04.s
63	17	1.2	296	32	AA366765	AA366765 EST77750	c 136	17	1.2	416	40	AA934113	AA934113 on95c02.s
64	17	1.2	298	45	AI351243	AI351243 qt47e05.x	c 137	17	1.2	417	22	R80915	R80915 y194f11.r1
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69	17	1.2	300	90	AQ073299	AQ073299 l(2)10607	c 142	17	1.2	420	48	AI580279	AI580279 tm45f11.x
70	17	1.2	303	59	AV094160	AV094160 AY094160	c 143	17	1.2	420	64	AW070916	AW070916 xa31d01.x
71	17	1.2	304	90	AQ025925	AQ025925 l(2)k1011	c 144	17	1.2	421	29	AA135786	AA135786 z111f08.r
72	17	1.2	308	62	AI905687	AI905687 IL-BT095-	c 145	17	1.2	423	49	AI657945	AI657945 fc18h12.y
73	17	1.2	312	28	AA092926	AA092926 m0611.seq	c 146	17	1.2	424	24	H73235	H73235 ya16f01.s1
74	17	1.2	312	28	AA092926	AA092926 m0611.seq	c 147	17	1.2	426	38	AA766295	AA766295 oa28f04.s

c 148	17	1.2	426	39	AA885212	AA885212	am34c12.s	221	17	1.2	511	35	AA562784	AA562784	vl44q03.r
c 149	17	1.2	427	43	AI214410	Q958b10.x		c 222	17	1.2	511	105	AQ665829	AQ665829	HS_5372_B
c 150	17	1.2	428	64	AI043943	DKSZP434F		c 223	17	1.2	512	51	AI713183	AI713183	UI-R-10-a
c 151	17	1.2	429	39	AA866878	nr90e06.s		c 224	17	1.2	513	103	AQ448485	AQ448485	mgxb0020F
c 152	17	1.2	430	39	AA864625	Qd45d04.s		c 225	17	1.2	516	39	AA876066	AA876066	OB93a09.s
c 153	17	1.2	431	44	AI305050	ESR00015		c 226	17	1.2	519	36	AA636495	AA636495	vr18e10.r
c 154	17	1.2	432	26	W72838	W72838	zds57g12.s1	c 227	17	1.2	520	37	AI719302	AI719302	zh35b11.s
c 155	17	1.2	433	40	AA928684	AA928684	On48f04.s	c 228	17	1.2	522	60	AI796182	AI796182	wh43f05.x
c 156	17	1.2	434	24	H78162	H78162	yu86b10.r1	c 229	17	1.2	523	100	AQ295445	AQ295445	HS_3034_B
c 157	17	1.2	435	26	W72837	W72837	zds57g12.s1	c 230	17	1.2	527	73	AW167553	AW167553	xn55902.x
c 158	17	1.2	436	63	AW062216	AW062216	wz93g03.x	c 231	17	1.2	530	88	AQ848057	AQ848057	LMAJFV1_1
c 159	17	1.2	437	74	AW192193	AW192193	x181c08.x	c 232	17	1.2	537	102	AQ376675	AQ376675	RPCI-11-1
c 160	17	1.2	438	43	AI203438	AI203438	qr25d08.x	c 233	17	1.2	543	48	AI591148	AI591148	tw86a04.x
c 161	17	1.2	438	44	AI261769	AI261769	qk10c02.x	c 234	17	1.2	544	79	CNS00N6L	AL081531	ArabiDops
c 162	17	1.2	440	41	AI058424	AI058424	UI-R-C1-k	c 235	17	1.2	551	105	AQ663921	AQ663921	HS_2171_B
c 163	17	1.2	442	44	AI292334	AI292334	qm77b10.x	c 236	17	1.2	552	43	AI102258	AI102258	EST211547
c 164	17	1.2	442	88	AQ849884	AQ849884	LMAJFV1_1	c 237	17	1.2	554	38	AA743709	AA743709	ny92f03.s
c 165	17	1.2	443	42	AI127172	AI127172	qb99a08.x	c 238	17	1.2	554	63	AI955196	AI955196	wx31b04.x
c 166	17	1.2	445	45	AI332427	AI332427	qq45a12.x	c 239	17	1.2	557	45	AI378295	AI378295	tc43h09.x
c 167	17	1.2	446	43	AI1185820	AI1185820	qe49h04.x	c 240	17	1.2	557	88	AQ855270	AQ855270	CPg1897A
c 168	17	1.2	447	38	AA745977	AA745977	Ob18g03.s	c 241	17	1.2	559	41	AI023165	AI023165	OW66C02.s
c 169	17	1.2	447	39	AA822994	AA822994	vw39d09.r	c 242	17	1.2	559	63	AW007110	AW007110	wt09C09.x
c 170	17	1.2	448	42	AI141722	AI141722	ot20a03.x	c 243	17	1.2	564	105	AQ655922	AQ655922	Sheared D
c 171	17	1.2	450	25	N62285	N62285	Y*90b12.s1	c 244	17	1.2	565	74	AV388115	AV388115	AV388115
c 172	17	1.2	450	63	AI943549	AI943549	BSBmF5Z4	c 245	17	1.2	569	64	AW042303	AW042303	614026G07
c 173	17	1.2	455	23	H50679	H50679	Yp86h01.s1	c 246	17	1.2	576	30	AA242244	AA242244	mw25c10.r
c 174	17	1.2	455	42	AI088801	AI088801	qa21d12.x	c 247	17	1.2	587	50	AI672891	AI672891	we73g06.x
c 175	17	1.2	455	45	AI351877	AI351877	qq21g04.x	c 248	17	1.2	590	105	AQ633932	AQ633932	RPCI-11-4
c 176	17	1.2	456	63	AW005143	AW005143	wv80c03.x	c 249	17	1.2	596	34	AA517392	AA517392	vh99h07.r
c 177	17	1.2	457	62	AI920700	AI920700	614026G07	c 250	17	1.2	600	74	AW175086	AW175086	Y132b02.y
c 178	17	1.2	457	63	AW005152	AW005152	wv80d02.x	c 251	17	1.2	602	43	AI179329	AI179329	ESY223024
c 179	17	1.2	457	72	AW162476	AW162476	au66g06.x	c 252	17	1.2	602	49	AI649752	AI649752	496009C09
c 180	17	1.2	458	27	AA0111980	AA0111980	TgESTZz17	c 253	17	1.2	613	39	AA872875	AA872875	Oh57h01.s
c 181	17	1.2	458	63	AI961364	AI961364	wcl7e03.x	c 254	17	1.2	622	28	AA099900	AA099900	zk87e09.r
c 182	17	1.2	459	29	AA160114	AA160114	zo86a10.r	c 255	17	1.2	625	28	AA098827	AA098827	zn45a02.r
c 183	17	1.2	459	33	AA424101	AA424101	zv80c05.r	c 256	17	1.2	631	36	AA660699	AA660699	00588 Mtr
c 184	17	1.2	459	41	AI062297	AI062297	GH01453.s	c 257	17	1.2	631	69	AW141292	AW141292	EST29133r
c 185	17	1.2	460	29	AA173647	AA173647	zp03h04.r	c 258	17	1.2	632	100	AQ287526	AQ287526	nbxb0030M
c 186	17	1.2	460	45	AI406459	AI406459	ESR233745	c 259	17	1.2	633	27	AA045236	AA045236	zk65g03.s
c 187	17	1.2	462	48	AI558834	AI558834	fb67a08.y	c 260	17	1.2	635	39	AA846530	AA846530	aj56f03.s
c 188	17	1.2	463	60	AI802061	AI802061	tx29h01.x	c 261	17	1.2	640	64	AW018930	AW018930	fd61h05.y
c 189	17	1.2	467	60	AI796951	AI796951	we25b10.x	c 262	17	1.2	640	105	AQ638249	AQ638249	927P1-11H
c 190	17	1.2	475	39	AA822985	AA822985	vw39c10.r	c 263	17	1.2	645	61	AL038359	AL038359	DKF2p566L
c 191	17	1.2	476	38	AA757252	AA757252	ah69c07.s	c 264	17	1.2	645	45	AA799313	AA799313	EST188810
c 192	17	1.2	472	64	AW028011	AW028011	wv61b09.x	c 265	17	1.2	671	100	AQ287833	AQ287833	nbxb0031M
c 193	17	1.2	472	99	AI96276	AI96276	RPCI11-61	c 266	17	1.2	692	105	AA641338	AA641338	RPCI93-Dp
c 194	17	1.2	474	48	AI545350	AI545350	fb74b12.y	c 267	17	1.2	736	61	AL037328	AL037328	DKF2p564E
c 195	17	1.2	475	48	AI566228	AI566228	tq70a09.x	c 268	17	1.2	737	104	AQ575421	AQ575421	nbxb0087E
c 196	17	1.2	476	39	AA822985	AA822985	vw39c10.r	c 269	17	1.2	710	82	AQ689558	AQ689558	nbxb0079L
c 197	17	1.2	476	100	AQ323168	AQ323168	RPCI11-10	c 270	17	1.2	712	43	AI176730	AI176730	EST220323
c 198	17	1.2	478	102	AQ349756	AQ349756	RPCI11-12	c 271	17	1.2	716	81	B77585	B77585	T27B24TR TA
c 199	17	1.2	479	35	AA583028	AA583028	nn80e02.s	c 272	17	1.2	733	80	AF075876	AF075876	Salmonell
c 200	17	1.2	480	33	AA401428	AA401428	zu68g03.s	c 273	17	1.2	736	61	AL037328	AL037328	DKF2p564E
c 201	17	1.2	480	63	AI988559	AI988559	sd04a07.y	c 274	17	1.2	737	104	AQ575421	AQ575421	nbxb0087E
c 202	17	1.2	483	48	AI592449	AI592449	vt08e07.y	c 275	17	1.2	751	64	AW027541	AW027541	wv74d09.x
c 203	17	1.2	484	39	AA823851	AA823851	vt08e07.r	c 276	17	1.2	752	49	AI664723	AI664723	TENG0864
c 204	17	1.2	485	22	R42167	R42167	Yf99e01.s1	c 277	17	1.2	753	42	AI092271	AI092271	oz37e05.x
c 205	17	1.2	485	88	AQ848618	AQ848618	LMAJFV1_1	c 278	17	1.2	759	89	AQ916509	AQ916509	nbab0065E
c 206	17	1.2	487	46	AI399464	AI399464	NCSF4G11T	c 279	17	1.2	762	100	AQ327052	AQ327052	nbxb0040G
c 207	17	1.2	489	48	AI549243	AI549243	UI-R-C3-t	c 280	17	1.2	762	61	AL038360	AL038360	DKF2p566L
c 208	17	1.2	492	34	AA469302	AA469302	nc68f04.s	c 281	17	1.2	778	63	AW013050	AW013050	ODt-0097
c 209	17	1.2	496	61	AL043942	AL043942	DKSZP434F	c 282	17	1.2	787	100	AQ292182	AQ292182	nbxb00402J
c 210	17	1.2	496	63	AI941514	AI941514	618030B03	c 283	17	1.2	835	34	AA522522	AA522522	nl38d02.s
c 211	17	1.2	498	46	AI417420	AI417420	tq30g07.x	c 284	17	1.2	919	79	CNS00CSW	AL059697	Drosophil
c 212	17	1.2	498	38	AQ875479	AQ875479	V125H1 mt	c 285	17	1.2	929	79	CNS008CZ	AL051517	Drosophil
c 213	17	1.2	499	39	AA897921	AA897921	NCM2E1T7	c 286	17	1.2	932	79	CNS0048C	AL066389	Drosophil
c 214	17	1.2	502	39	AA881220	AA881220	vx10c05.r	c 287	17	1.2	932	88	AQ890086	AQ890086	HS_4831_B
c 215	17	1.2	502	100	AQ300812	AQ300812	HS_2217_B	c 288	17	1.2	947	79	CNS00D31	AL060567	Drosophil
c 216	17	1.2	505	69	AW123020	AW123020	UI-M-BH2	c 289	16	1.1	52	43	AI203654	AI203654	qt48e05.x
c 217	17	1.2	506	69	AW141797	AW141797	ESR291890	c 290	16	1.1	112	104	AA587047	AA587047	RPCI-11-4
c 218	17	1.2	507	23	H50305	H50305	YQ28b12.r1	c 291	16	1.1	131	37	AA718057	AA718057	vt90f12.r
c 219	17	1.2	509	34	AA462995	AA462995	v970c04.r	c 292	16	1.1	167	64	AW074095	AW074095	xh07f03.x
c 220	17	1.2	509	88	AQ846560	AQ846560	LMAJFV1_1	c 293	16	1.1	185	37	R83937	R83937	15896 Lambd

294	16	1.1	188	26	W35479	W35479 139 Mouse V	C 367	16	1.1	320	48	AI582808	AI582808 tn36a05.x
295	16	1.1	193	103	A0485008	A0485008 RPCI-11-2	368	16	1.1	320	104	A0529847	A0529847 RPCI-11-3
296	16	1.1	195	59	AV093620	AV093620 AV093620	C 369	16	1.1	325	24	H82595	H82595 yv77907.r1
297	16	1.1	195	74	AW219735	AW219735 EST302217	C 370	16	1.1	325	20	Z25652	Z25652 ARTS1117 ve
298	16	1.1	200	42	AI149336	AI149336 qc76h03.x	C 371	16	1.1	327	32	AA366349	AA366349 EST77284
299	16	1.1	203	69	AV206565	AV206565 AV206565	C 372	16	1.1	331	90	AQ031642	AQ031642 HS_2225_B
300	16	1.1	211	102	A0403396	A0403396 HS_2257_B	C 373	16	1.1	331	90	AQ009196	AQ009196 CIT-HFP-2
301	16	1.1	213	25	N48947	N48947 yv76d10.r1	374	16	1.1	334	33	AA393011	AA393011 LD03296.5
302	16	1.1	214	31	AA308883	AA308883 EST179687	375	16	1.1	337	27	AA038448	AA038448 m92a07.r
303	16	1.1	216	50	AI708431	AI708431 as97b12.x	376	16	1.1	337	60	AV119872	AV119872 AV119872
304	16	1.1	218	71	AV256058	AV256058 AV256058	377	16	1.1	338	39	AA833189	AA833189 ud02h03.r
305	16	1.1	219	50	AV039825	AV039825 AV039825	378	16	1.1	339	90	AQ070924	AQ070924 HS_2268_A
306	16	1.1	219	88	AQ046781	AQ046781 LMAJFV1.1	C 379	16	1.1	342	29	AA142321	AA142321 JM00M038.
307	16	1.1	220	61	AV155909	AV155909 AV155909	380	16	1.1	345	34	C25363	C25363 C25363 R1ce
308	16	1.1	229	59	AV067339	AV067339 AV067339	381	16	1.1	345	82	AQ676784	AQ676784 HS_5456_B
309	16	1.1	235	70	AV241809	AV241809 AV241809	382	16	1.1	347	40	AA951481	AA951481 LD31959.5
310	16	1.1	237	39	AA885632	AA885632 Oj32a10.s	383	16	1.1	347	62	AV188650	AV188650 AV188650
311	16	1.1	241	63	AI946380	AI946380 bs24f07.y	C 384	16	1.1	347	63	AI945870	AI945870 bs17909.y
312	16	1.1	242	43	C99795	C99795 C99795 YAC	C 385	16	1.1	349	59	AV117032	AV117032 AV117032
313	16	1.1	242	74	AV380962	AV380962 AV380962	C 386	16	1.1	351	81	B54075	B54075 CIT-HSP-201
314	16	1.1	243	20	TI4448	TI4448 SMEST0109.S	387	16	1.1	353	30	AA201832	AA201832 LD03743.5
315	16	1.1	243	72	AV292919	AV292919 AV292919	C 388	16	1.1	353	47	AI467932	AI467932 tj84c04.x
316	16	1.1	246	30	AA266274	AA266274 mz63f05.r	C 389	16	1.1	355	21	R14564	R14564 yf83e10.r1
317	16	1.1	247	34	AA466846	AA466846 ve92q09.r	390	16	1.1	356	33	AA391750	AA391750 LD10801.5
318	16	1.1	249	74	AV376746	AV376746 AV376746	C 391	16	1.1	357	88	AQ841300	AQ841300 T136443b
319	16	1.1	252	73	AV338944	AV338944 AV338944	C 392	16	1.1	357	91	AQ091904	AQ091904 HS_3014_B
320	16	1.1	254	48	AI572526	AI572526 te38h07.x	393	16	1.1	358	20	Z43649	Z43649 HSC1HF091.n
321	16	1.1	254	71	AV323763	AV323763 AV323763	C 394	16	1.1	358	23	H41275	H41275 yp67b11.s1
322	16	1.1	255	24	H97184	H97184 yx03h09.s1	C 395	16	1.1	358	44	AI308725	AI308725 SMOVAFCAP
323	16	1.1	258	29	AA127054	AA127054 zn28f09.s	C 396	16	1.1	359	81	B76220	B76220 RPCI11-14A1
324	16	1.1	259	59	AV095548	AV095548 AV095548	C 397	16	1.1	360	36	C62190	C62190 C62190 YuJ1
325	16	1.1	262	21	T97160	T97160 ye50c12.r1	398	16	1.1	360	36	C66985	C66985 C66985 YuJ1
326	16	1.1	262	28	CI5514	CI5514 CI5514 Clon	399	16	1.1	361	51	AI750952	AI750952 cn06g02.y
327	16	1.1	266	71	AV278197	AV278197 AV278197	400	16	1.1	361	51	AA439053	AA439053 LD13491.5
328	16	1.1	267	100	AQ264612	AQ264612 CITBI-E1-	401	16	1.1	362	43	AI220074	AI220074 qg84d10.x
329	16	1.1	269	59	AV082003	AV082003 AV082003	C 402	16	1.1	363	21	T66808	T66808 ya50a11.r1
330	16	1.1	271	34	AA489615	AA489615 ae32h12.r	C 403	16	1.1	363	23	H42280	H42280 yo63d01.r1
331	16	1.1	272	70	AW154961	AW154961 614092H12	C 404	16	1.1	365	36	AA639273	AA639273 ns04h10.r
332	16	1.1	273	73	AV341111	AV341111 AV341111	C 405	16	1.1	365	79	FR0009261	FR0009261 F.rubripe
333	16	1.1	274	36	C73800	C73800 C73800 Rice	C 406	16	1.1	369	81	BS0113	BS0113 C17978SK-44
334	16	1.1	277	51	AV052860	AV052860 AV052860	C 407	16	1.1	370	21	T84502	T84502 yd49f04.r1
335	16	1.1	278	71	AV268822	AV268822 AV268822	C 408	16	1.1	372	45	AI396263	AI396263 487013F10
336	16	1.1	279	38	AA772123	AA772123 a140c12.s	C 409	16	1.1	373	38	AA541038	AA541038 LD20821.5
337	16	1.1	279	49	AV014484	AV014484 AV014484	410	16	1.1	373	40	Z19071	Z19071 HSDHEB09.S
338	16	1.1	279	50	AV039520	AV039520 AV039520	C 411	16	1.1	373	46	AI418991	AI418991 tf43e08.x
339	16	1.1	280	82	AQ667091	AQ667091 HS_2107_A	C 412	16	1.1	373	62	AI928292	AI928292 wp12a08.x
340	16	1.1	281	72	AV300420	AV300420 AV300420	C 413	16	1.1	374	44	AI323838	AI323838 mt66b10.x
341	16	1.1	283	62	AV177297	AV177297 AV177297	C 414	16	1.1	374	61	AI827625	AI827625 wf32b10.x
342	16	1.1	284	29	AA127053	AA127053 zn28f09.r	C 415	16	1.1	375	21	T93973	T93973 ye29a04.r1
343	16	1.1	284	39	AA882981	AA882981 TENS0558	416	16	1.1	376	64	AW091328	AW091328 614092H12
344	16	1.1	284	39	AI855565	AI855565 sb38a05.y	C 417	16	1.1	379	47	AI490102	AI490102 EST248441
345	16	1.1	284	72	AV290599	AV290599 AV290599	418	16	1.1	380	27	C09398	C09398 C09398 YuJ1
346	16	1.1	285	23	R97430	R97430 yq53h01.s1	419	16	1.1	380	41	AI019143	AI019143 ub20a09.r
347	16	1.1	286	62	AI874226	AI874226 tz63a05.x	420	16	1.1	381	100	AQ297279	AQ297279 HS_3051_A
348	16	1.1	287	72	AW162174	AW162174 au89f03.y	C 421	16	1.1	382	62	AI988249	AI988249 EST267692
349	16	1.1	288	69	AV214645	AV214645 AV214645	C 422	16	1.1	385	29	AA133576	AA133576 zol14f12.r
350	16	1.1	290	60	AV139975	AV139975 AV139975	C 423	16	1.1	386	21	R17172	R17172 yg11a06.r1
351	16	1.1	293	60	AV119054	AV119054 AV119054	C 424	16	1.1	386	43	AI193885	AI193885 qe80e06.x
352	16	1.1	296	59	AV118435	AV118435 AV118435	C 425	16	1.1	387	21	T80606	T80606 yd23f01.s1
353	16	1.1	297	60	AV118938	AV118938 AV118938	426	16	1.1	388	33	AA442642	AA442642 zv59g10.r
354	16	1.1	297	64	AW089750	AW089750 xd07e12.x	427	16	1.1	388	42	AI094749	AI094749 qe08h11.x
355	16	1.1	301	48	AW055630	AW055630 AW055630	428	16	1.1	388	81	B87719	B87719 RPT111-30D1
356	16	1.1	303	79	CNS0006Q	AL082832 Arabidops	429	16	1.1	389	47	AI494189	AI494189 t114h02.y
357	16	1.1	304	69	AW135710	AW135710 OI-H-B11-	430	16	1.1	389	64	AW017204	AW017204 EST272626
358	16	1.1	304	81	B83478	B83478 RPCI11-15C2	C 431	16	1.1	389	72	AW163868	AW163868 614092H12
359	16	1.1	309	91	AQ091110	AQ091110 HS_3007.B	C 432	16	1.1	391	47	AI488400	AI488400 EST246722
360	16	1.1	311	69	AV215348	AV215348 AV215348	C 433	16	1.1	393	35	AA538848	AA538848 LD18470.5
361	16	1.1	312	31	AA308981	AA308981 EST179788	C 434	16	1.1	393	39	AA538203	AA538203 LD23606.5
362	16	1.1	313	62	AI928295	AI928295 wp12a11.x	435	16	1.1	393	87	AQ772752	AQ772752 HS_2019_B
363	16	1.1	314	41	AU007657	AU007657 AU007657	436	16	1.1	393	99	AQ235351	AQ235351 HS_2035_A
364	16	1.1	315	105	AQ640238	AQ640238 927P1-2F6	437	16	1.1	394	88	AQ854618	AQ854618 nbx0800J
365	16	1.1	317	87	AQ817313	AQ817313 HS_5281_A	438	16	1.1	398	34	AA472480	AA472480 v107b03.r
366	16	1.1	320	42	AI099654	AI099654 34380 Lam	C 439	16	1.1	398	37	T43614	T43614 6877 Lambda

c 440	16	1.1	399	31	AA286767	AA286767	zs51d06.r	c 513	16	1.1	464	42	AI083728	AI083728	gf19q03.x
c 441	16	1.1	400	46	AI399304	AI399304	NCW07A3T3	c 514	16	1.1	464	74	AW201529	AW201529	sf04c04.y
c 442	16	1.1	401	29	AA154765	AA154765	mt66b10.r	c 515	16	1.1	464	91	AQ126320	AQ126320	HS_3037.B
c 443	16	1.1	402	42	AI118748	AI118748	uc13a06.r	c 516	16	1.1	465	46	AA998141	AA998141	UI-R-C0-1
c 444	16	1.1	403	91	AQ115777	AQ115777	RPC1111.52	c 517	16	1.1	467	30	AA212334	AA212334	mu78e05.r
c 445	16	1.1	404	26	W97216	W97216	mg08e02.r1	c 518	16	1.1	467	47	AI510465	AI510465	mp97d09.y
c 446	16	1.1	404	34	AA536616	AA536616	LD17388.5	c 519	16	1.1	467	88	AQ866488	AQ866488	nbe00028M
c 447	16	1.1	405	64	AI120877	AI120877	DKFP762L	c 520	16	1.1	468	46	AI461125	AI461125	sa75a03.y
c 448	16	1.1	405	90	AQ1016864	AQ1016864	CIT-HSP-2	c 521	16	1.1	469	34	AA458650	AA458650	aa16c07.s
c 449	16	1.1	407	42	AI146879	AI146879	QY22g09.s	c 522	16	1.1	469	74	AI362952	AI362952	gf07f02.y
c 450	16	1.1	408	30	AA203034	AA203034	LD00496.5	c 523	16	1.1	470	45	AW084586	AW084586	wg26h09.x
c 451	16	1.1	408	81	B62642	B62642	T22M16TF.TA	c 524	16	1.1	470	64	AQ081958	AQ081958	HS_5323.A
c 452	16	1.1	409	40	AA965984	AA965984	r8g07a1.r	c 525	16	1.1	470	88	AQ881958	AQ881958	HS_5323.A
c 453	16	1.1	413	87	AQ794203	AQ794203	nbxb0052E	c 526	16	1.1	473	47	AI488044	AI488044	EST246366
c 454	16	1.1	415	74	AV393174	AV393174	AV393174	c 527	16	1.1	473	91	AQ109936	AQ109936	CIT-HSP-2
c 455	16	1.1	415	21	AQ090792	AQ090792	HS_3011.B	c 528	16	1.1	474	39	AA824610	AA824610	oc83f11.s
c 456	16	1.1	416	24	H63134	H63134	yr48g04.s1	c 529	16	1.1	474	48	AI622223	AI622223	486038B04
c 457	16	1.1	416	60	AI800154	AI800154	tr23a08.x	c 530	16	1.1	476	25	N70411	N70411	zg61b11.s1
c 458	16	1.1	417	90	AQ045104	AQ045104	RPC1111-34	c 531	16	1.1	476	47	AI513631	AI513631	LD45833.5
c 459	16	1.1	418	27	AA049953	AA049953	mj38e11.r	c 532	16	1.1	477	45	AI338219	AI338219	qt41f05.x
c 460	16	1.1	418	62	AI878079	AI878079	fc57b11.y	c 533	16	1.1	477	99	AQ233981	AQ233981	HS_2053.A
c 461	16	1.1	419	27	AA049960	AA049960	mj38g11.r	c 534	16	1.1	478	40	AA949961	AA949961	LD28343.5
c 462	16	1.1	419	45	AI383412	AI383412	lc97a08.x	c 535	16	1.1	478	60	AV119858	AV119858	AV119858
c 463	16	1.1	420	31	AA310554	AA310554	EST181358	c 536	16	1.1	479	74	AV396004	AV396004	AV396004
c 464	16	1.1	420	62	AI894692	AI894692	EST284135	c 537	16	1.1	479	99	AQ208862	AQ208862	HS_3056.B
c 465	16	1.1	422	50	AI699292	AI699292	wa67a04.x	c 538	16	1.1	480	29	AA158523	AA158523	z072d09.s
c 466	16	1.1	422	100	AQ321950	AQ321950	LMAJFV1.1	c 539	16	1.1	480	41	AI035516	AI035516	ub48g11.r
c 467	16	1.1	424	88	AQ852769	AQ852769	LMAJFV1.1	c 540	16	1.1	481	47	AI475830	AI475830	tc87a09.x
c 468	16	1.1	426	31	AA822606	AA822606	zs9a005.r	c 541	16	1.1	481	47	AI516685	AI516685	LD42655.5
c 469	16	1.1	427	23	H41411	H41411	yp72c05.s1	c 542	16	1.1	481	81	B44856	B44856	HS-1060-A1-
c 470	16	1.1	427	40	AA922280	AA922280	Om46g11.s	c 543	16	1.1	481	81	B44856	B44856	HS-1060-A1-
c 471	16	1.1	427	88	AQ89542	AQ89542	HS_3188.B	c 544	16	1.1	482	62	AI456208	AI456208	LD36079.5
c 472	16	1.1	428	43	AI225101	AI225101	q132f03.x	c 545	16	1.1	482	62	AI899810	AI899810	SP94b01.y
c 473	16	1.1	429	36	AA632061	AA632061	nb70e09.s	c 546	16	1.1	483	62	AI927347	AI927347	wn49f03.x
c 474	16	1.1	429	39	AQ206905	AQ206905	HS_3238.B	c 547	16	1.1	484	21	R10794	R10794	yf36e02.r1
c 475	16	1.1	433	62	AI894670	AI894670	EST264113	c 548	16	1.1	485	46	AI405307	AI405307	GH25264.5
c 476	16	1.1	434	69	AA812252	AA812252	nr82b11.s	c 549	16	1.1	487	21	T83350	T83350	ye03d02.s1
c 477	16	1.1	434	69	AA383024	AA383024	AV383024	c 550	16	1.1	487	23	H49657	H49657	y023a04.r1
c 478	16	1.1	434	99	AQ234513	AQ234513	HS_2052.B	c 551	16	1.1	488	68	AQ849736	AQ849736	LMAJFV1.1
c 479	16	1.1	435	22	R25683	R25683	Yg44c12.r2	c 552	16	1.1	489	99	AI976899	AI976899	EST271581
c 480	16	1.1	437	104	AQ517442	AQ517442	HS_5119.B	c 553	16	1.1	489	103	AQ502171	AQ502171	V8B11.mtn
c 481	16	1.1	438	25	W04974	W04974	za42d01.r1	c 554	16	1.1	490	40	AA940893	AA940893	LD23215.5
c 482	16	1.1	438	82	AQ737932	AQ737932	HS_2017.B	c 555	16	1.1	490	102	AQ399124	AQ399124	mgxb0006F
c 483	16	1.1	439	21	T80697	T80697	yd32c04.r1	c 556	16	1.1	491	104	AQ507046	AQ507046	HS_5355.B
c 484	16	1.1	439	41	AI047675	AI047675	uh81f04.r	c 557	16	1.1	492	104	AQ507046	AQ507046	HS_5355.B
c 485	16	1.1	439	42	AF074726	AF074726	AF074726	c 558	16	1.1	492	105	AQ512864	AQ512864	HS_5116.A
c 486	16	1.1	439	48	AI566932	AI566932	tn25b02.x	c 559	16	1.1	493	82	AQ692599	AQ692599	zvi9g12.r
c 487	16	1.1	439	64	AW083818	AW083818	xc35f02.x	c 560	16	1.1	494	38	AA785424	AA785424	g7c05a1.r
c 488	16	1.1	439	104	AQ561655	AQ561655	HS_5206.A	c 561	16	1.1	494	39	AA902079	AA902079	NCP5E57
c 489	16	1.1	440	88	AQ852393	AQ852393	LMAJFV1.1	c 562	16	1.1	494	88	AQ848684	AQ848684	LMAJFV1.1
c 490	16	1.1	441	21	R20975	R20975	Yg06g08.r1	c 563	16	1.1	495	40	AA948788	AA948788	LD27419.5
c 491	16	1.1	442	34	AA532899	AA532899	nj18d05.s	c 564	16	1.1	495	79	FR0023707	FR0023707	F_rubripe
c 492	16	1.1	443	25	N77807	N77807	zb16a04.s1	c 565	16	1.1	497	26	W47960	W47960	mc87d01.r1
c 493	16	1.1	445	23	H44640	H44640	YD20a05.r1	c 566	16	1.1	497	38	AA392315	AA392315	LD11140.5
c 494	16	1.1	448	29	AA178472	AA178472	mt16f07.r	c 567	16	1.1	497	38	AA788270	AA788270	r6d05a1.r
c 495	16	1.1	448	31	AA291297	AA291297	zs18e07.s	c 568	16	1.1	498	40	AA949851	AA949851	LD29895.5
c 496	16	1.1	448	87	AQ777821	AQ777821	HS_2024.B	c 569	16	1.1	498	74	AV394515	AV394515	AV394515
c 497	16	1.1	449	105	AQ660706	AQ660706	Sheared.D	c 570	16	1.1	498	74	AW205581	AW205581	UI-R-B11-
c 498	16	1.1	450	44	AI298185	AI298185	qm92h02.x	c 571	16	1.1	500	36	AA641620	AA641620	nr80a07.s
c 499	16	1.1	450	47	AI542799	AI542799	SD09264.5	c 572	16	1.1	501	100	AQ340412	AQ340412	nr80a07.s
c 500	16	1.1	451	30	AA258248	AA258248	zs33e07.s	c 573	16	1.1	502	48	AI560775	AI560775	tn22c02.x
c 501	16	1.1	452	37	AA704897	AA704897	zj82a05.s	c 574	16	1.1	504	64	AW019258	AW019258	fd61f12.x
c 502	16	1.1	455	25	N95938	N95938	yy76c07.s1	c 575	16	1.1	504	87	AQ786429	AQ786429	HS_3193.B
c 503	16	1.1	455	42	AI123667	AI123667	co16d02.x	c 576	16	1.1	504	88	AQ853015	AQ853015	LMAJFV1.1
c 504	16	1.1	457	30	AA214786	AA214786	md81c07.r	c 577	16	1.1	504	99	AQ172611	AQ172611	HS_3197.A
c 505	16	1.1	457	39	AA820459	AA820459	LD24202.5	c 578	16	1.1	504	100	AQ302145	AQ302145	HS_3186.B
c 506	16	1.1	457	39	C85918	C85918	C85918	c 579	16	1.1	504	103	AQ425525	AQ425525	CITB1-E1-
c 507	16	1.1	458	82	AQ713878	AQ713878	HS_2129.B	c 580	16	1.1	505	62	AI891122	AI891122	wn28g10.x
c 508	16	1.1	458	100	AQ316940	AQ316940	CITB1-E1-	c 581	16	1.1	506	103	AQ447504	AQ447504	mgxb0007L
c 509	16	1.1	459	31	AA287068	AA287068	zt20d08.r	c 582	16	1.1	507	44	AT262484	AT262484	qk41c12.x
c 510	16	1.1	459	39	AA846382	AA846382	aj55e05.s	c 583	16	1.1	507	74	AV394960	AV394960	AV394960
c 511	16	1.1	460	45	AA859439	AA859439	UI-R-A0-b	c 584	16	1.1	508	99	AQ193332	AQ193332	HS_3065.A
c 512	16	1.1	462	23	H39685	H39685	y052c06.r1	c 585	16	1.1	508	99	AQ193332	AQ193332	HS_3065.A

586	16	1.1	510	82	AQ694541	HS_5485_A	c	659	16	1.1	545	103	AQ505255	RPC1-11-1	AQ505255	RPC1-11-1
587	16	1.1	512	40	AA988109	OS07a12_s		660	16	1.1	546	46	AI398952	NCW06H8T7	AI398952	NCW06H8T7
588	16	1.1	512	74	AV394283	AV394283		661	16	1.1	546	105	AQ664200	HS_5496_B	AQ664200	HS_5496_B
589	16	1.1	514	47	AI278442	qm53801.x		662	16	1.1	547	34	AA495228	fa01e11.r	AA495228	fa01e11.r
590	16	1.1	514	47	AI494909	sa92802.y		663	16	1.1	547	74	AV390614	AV390614	AV390614	AV390614
591	16	1.1	514	62	AI886863	wk29e12.x		664	16	1.1	548	74	AV388006	AV388006	AV388006	AV388006
592	16	1.1	514	81	B27698	T103TRB_TA		665	16	1.1	549	46	AI427284	mc87d01.y	AI427284	mc87d01.y
593	16	1.1	515	61	AI813494	wf64f04.x		666	16	1.1	551	38	AA440626	LD15467_5	AA440626	LD15467_5
594	16	1.1	515	74	AW200000	da10405.y		667	16	1.1	551	50	AI673347	tw35a01.x	AI673347	tw35a01.x
595	16	1.1	515	104	AQ526647	HS_5193_A		668	16	1.1	552	103	AQ458526	HS_5061_A	AQ458526	HS_5061_A
596	16	1.1	516	100	AQ260464	CITBI-EI-		669	16	1.1	553	44	AI294871	LP08095_5	AI294871	LP08095_5
597	16	1.1	516	103	AQ459533	HS_5085_A		670	16	1.1	554	44	AI255479	ui86a10.x	AI255479	ui86a10.x
598	16	1.1	516	104	AQ526174	HS_5312_B		671	16	1.1	555	62	AI881887	606074F06	AI881887	606074F06
599	16	1.1	517	63	AI963493	wf64a05.x		672	16	1.1	556	46	AI401887	GJ02955_3	AI401887	GJ02955_3
600	16	1.1	517	74	AV386565	AV386565		673	16	1.1	558	34	AA533105	n19h04_s	AA533105	n19h04_s
601	16	1.1	517	74	AV394940	AV394940		674	16	1.1	558	47	AI512956	LD45123_5	AI512956	LD45123_5
602	16	1.1	518	34	AA464810			675	16	1.1	558	48	AI526628	SD09441_5	AI526628	SD09441_5
603	16	1.1	519	102	AQ405413			676	16	1.1	558	74	AV391979	AV391979	AV391979	AV391979
604	16	1.1	520	25	N78279			677	16	1.1	558	90	AQ047197	RPC111-35	AQ047197	RPC111-35
605	16	1.1	520	39	AA820906	LD24841_5		678	16	1.1	559	64	AW043232	ST30H04_P	AW043232	ST30H04_P
606	16	1.1	520	41	AI069876	TENU2924		679	16	1.1	559	103	AQ497560	HS_5210_B	AQ497560	HS_5210_B
607	16	1.1	520	74	AW172976	x123e12.x		680	16	1.1	560	38	AA804959	rk97h11_s	AA804959	rk97h11_s
608	16	1.1	521	36	AA625317	a71802.r		681	16	1.1	560	38	AA802050	GM03778_5	AA802050	GM03778_5
609	16	1.1	521	38	AA539345	LD17436_5		682	16	1.1	562	88	AQ837078	HS_5464_A	AQ837078	HS_5464_A
610	16	1.1	521	46	AI399486	NCSP6A6T7		683	16	1.1	563	88	AQ841299	T136442b	AQ841299	T136442b
611	16	1.1	521	47	AI518349	LD37835_5		684	16	1.1	564	47	AI519614	LD39262_5	AI519614	LD39262_5
612	16	1.1	523	34	AA482546	zt34b01.s		685	16	1.1	564	48	AI564755	td18g04.x	AI564755	td18g04.x
613	16	1.1	523	34	AA482546	zt34b01.s		686	16	1.1	565	100	AQ322154	RPC111-10	AQ322154	RPC111-10
614	16	1.1	523	90	AQ077612	CIT-HSP-2		687	16	1.1	568	100	AQ335251	HS_5014_B	AQ335251	HS_5014_B
615	16	1.1	524	45	AI360257	qy84g03.x		688	16	1.1	569	74	AJ273352	AJ273352	AJ273352	AJ273352
616	16	1.1	524	47	AI485718	EST244039		689	16	1.1	570	74	AV391088	AV391088	AV391088	AV391088
617	16	1.1	524	47	AI520534	LD40723_5		690	16	1.1	572	42	AI135047	GH13661_5	AI135047	GH13661_5
618	16	1.1	524	62	AI902162	618014H09		691	16	1.1	572	90	AQ063554	HS_2183_A	AQ063554	HS_2183_A
619	16	1.1	525	42	AU023596			692	16	1.1	573	64	AW032970	EST276529	AW032970	EST276529
620	16	1.1	526	21	RI1810	yf53a01.r1		693	16	1.1	574	47	AI512200	LD43960_5	AI512200	LD43960_5
621	16	1.1	526	79	CNSNOEX			694	16	1.1	575	44	AI294207	LP07528_5	AI294207	LP07528_5
622	16	1.1	527	74	AV386733	AV386733		695	16	1.1	575	63	AI939408	qy84g03.x	AI939408	qy84g03.x
623	16	1.1	527	74	AV393077	AV393077		696	16	1.1	575	82	AQ0729014	HS_5466_B	AQ0729014	HS_5466_B
624	16	1.1	528	36	AA607436	vc041f12.r		697	16	1.1	576	44	AI294573	LP07978_5	AI294573	LP07978_5
625	16	1.1	528	37	AA651422			698	16	1.1	577	40	AA950599	LD30457_5	AA950599	LD30457_5
626	16	1.1	528	37	AA651422			699	16	1.1	577	46	AA138472	td10361_5	AA138472	td10361_5
627	16	1.1	528	64	AW017351			700	16	1.1	577	50	AI678875	tu70c11.x	AI678875	tu70c11.x
628	16	1.1	528	105	AQ647196	EST272773		701	16	1.1	577	62	AI897808	EST267251	AI897808	EST267251
629	16	1.1	530	44	AI281716	RPC193-Dp		702	16	1.1	577	87	AQ0757221	HS_3482_A	AQ0757221	HS_3482_A
630	16	1.1	530	47	AI485147	qT37a11.x		703	16	1.1	577	104	AQ547174	RPC1-11-4	AQ547174	RPC1-11-4
631	16	1.1	530	88	AQ873935	EST243451		704	16	1.1	577	105	AQ623226	HS_5351_B	AQ623226	HS_5351_B
632	16	1.1	531	47	AI512222	V84A5_mrn		705	16	1.1	578	46	AI456712	LD36828_5	AI456712	LD36828_5
633	16	1.1	531	103	AQ493575	HS_5051_A		706	16	1.1	578	47	AI489237	EST247576	AI489237	EST247576
634	16	1.1	532	40	AA953832	OC08f08.s		707	16	1.1	578	51	AI711721	605060F11	AI711721	605060F11
635	16	1.1	533	64	AW034027	EST277689		708	16	1.1	579	91	AI162243	mgxb00131	AI162243	mgxb00131
636	16	1.1	533	74	AW205345	UT-H-B11-		709	16	1.1	580	44	AI297207	LP111463_5	AI297207	LP111463_5
637	16	1.1	533	100	AQ322326	RPC111-10		710	16	1.1	581	38	AA441011	LD15755_5	AA441011	LD15755_5
638	16	1.1	533	105	AQ653184			711	16	1.1	581	38	AA441011	LD15755_5	AA441011	LD15755_5
639	16	1.1	534	31	AA314858	Sheared_D		712	16	1.1	583	34	AA510274	VH58007.r	AA510274	VH58007.r
640	16	1.1	534	42	AI085589	EST186677		713	16	1.1	583	82	AQ694504	HS_5485_A	AQ694504	HS_5485_A
641	16	1.1	534	45	AI377819	oy68g11.x		714	16	1.1	584	28	AA116331	mp97d09.r	AA116331	mp97d09.r
642	16	1.1	534	45	AI377819	te58c09.x		715	16	1.1	584	28	AA1260647	LP04595_5	AA1260647	LP04595_5
643	16	1.1	534	46	AI436766	tb77g09.x		716	16	1.1	588	102	AQ365014	nbxb00621	AQ365014	nbxb00621
644	16	1.1	535	26	W30805			717	16	1.1	589	47	AI514380	LD40864_5	AI514380	LD40864_5
645	16	1.1	535	33	AA425119	X30805_zb78b02.r1		718	16	1.1	590	33	AA440760	LD15633_5	AA440760	LD15633_5
646	16	1.1	535	39	AA897310	zV47c12.r		719	16	1.1	596	33	AA410754	SV39b06.r	AA410754	SV39b06.r
647	16	1.1	536	38	AA391189	LD09284_5		720	16	1.1	596	47	AI543708	LD10584_5	AI543708	LD10584_5
648	16	1.1	536	45	AI356371	q221c07.x		721	16	1.1	598	67	AW079515	xcl8a11.x	AW079515	xcl8a11.x
649	16	1.1	537	70	AW146776	614085A07		722	16	1.1	599	87	AW0789461	HS_3171_A	AW0789461	HS_3171_A
650	16	1.1	539	104	AQ578870	nbxb00093H		723	16	1.1	600	25	N53467	yv41h09.s1	N53467	yv41h09.s1
651	16	1.1	540	81	B68349			724	16	1.1	600	28	AA062231	mL59g12.r	AA062231	mL59g12.r
652	16	1.1	542	47	AI519613	CIT-HSP-202		725	16	1.1	600	44	AI257784	LP06256_5	AI257784	LP06256_5
653	16	1.1	542	74	AV391117			726	16	1.1	600	45	AI353076	zeh0004.s	AI353076	zeh0004.s
654	16	1.1	542	102	AQ357587	CITBI-EI-		727	16	1.1	604	47	AI469386	tm08b02.x	AI469386	tm08b02.x
655	16	1.1	543	63	AI197339	701553434		728	16	1.1	605	44	AQ640327	927p1-18D	AQ640327	927p1-18D
656	16	1.1	544	49	AI638564	ts50b01.x		729	16	1.1	606	59	AI780154	EST261033	AI780154	EST261033
657	16	1.1	544	74	AJ273028			730	16	1.1	606	90	AQ081462	CIT-HSP-2	AQ081462	CIT-HSP-2
658	16	1.1	545	35	AA578929	nf30c08.s		731	16	1.1	607	47	AI542212	SD08360_5	AI542212	SD08360_5
659	16	1.1	545	102	AQ421972	RPC1-11-1										

732	16	1.1	608	44	AI296164	AI296164	LP09993.5	805	16	1.1	699	74	AW179970	AW179970	AW179970	MgA0022f
733	16	1.1	610	35	AA611995	AA611995	VO94C10.r	806	16	1.1	700	74	AW179998	AW179998	AW179998	MgA0052f
734	16	1.1	610	38	AA392637	AA392637	LD12870.5	807	16	1.1	702	51	AI731186	AI731186	AI731186	BNLGH1885
735	16	1.1	610	47	AI533343	AI533343	SD05122.5	808	16	1.1	706	42	AI110602	AI110602	AI110602	HA0028 Hu
736	16	1.1	610	63	AI1977518	AI1977518	EST272112	809	16	1.1	706	49	AF062710	AF062710	AF062710	AF062710
737	16	1.1	610	70	AW157233	AW157233	au93b08.x	810	16	1.1	711	44	AI290800	AI290800	qml13c02.x	AI290800
738	16	1.1	611	40	AA950861	AA950861	LD31012.5	811	16	1.1	711	105	AQ646949	AQ646949	RPCI93-Dp	AQ646949
739	16	1.1	611	63	AI967120	AI967120	61400603	812	16	1.1	717	99	AQ197771	AQ197771	CIT-HSP-2	AQ197771
740	16	1.1	612	69	AV384344	AV384344	AV384344	813	16	1.1	718	33	AA392700	AA392700	LD11802.5	AA392700
741	16	1.1	613	61	AI833597	AI833597	605092F08	814	16	1.1	721	99	AQ254925	AQ254925	LD15C22.T7	AQ254925
742	16	1.1	613	63	AI980446	AI980446	pat.pk002	815	16	1.1	731	40	AA949701	AA949701	LD29683.5	AA949701
743	16	1.1	614	44	AI297651	AI297651	LP11996.5	816	16	1.1	732	45	AU006052	AU006052	AU006052	AU006052
744	16	1.1	614	47	AI297651	AI297651	LP11996.5	817	16	1.1	732	99	AQ254924	AQ254924	B83B18.T	AQ254924
745	16	1.1	615	91	AI0158369	AI0158369	nbx000110	818	16	1.1	736	63	AI937005	AI937005	wp72a03.x	AI937005
746	16	1.1	617	34	AA536257	AA536257	LD16756.5	819	16	1.1	737	41	AF072312	AF072312	AF072312	AF072312
747	16	1.1	619	45	AI387441	AI387441	GHI7970.5	820	16	1.1	740	88	AQ864513	AQ864513	nb5b0023M	AQ864513
748	16	1.1	619	46	AI404321	AI404321	GH23975.5	821	16	1.1	744	47	AI523536	AI523536	th08a05.x	AI523536
749	16	1.1	620	30	AA246990	AA246990	LD06086.5	822	16	1.1	744	62	AI885857	AI885857	w162e06.x	AI885857
750	16	1.1	620	39	AA827922	AA827922	od08b07.s	823	16	1.1	744	91	AQ160219	AQ160219	mgxb0003F	AQ160219
751	16	1.1	620	105	AQ649892	AQ649892	Sheared.D	824	16	1.1	745	30	AA246213	AA246213	LD06002.5	AA246213
752	16	1.1	621	44	AI295123	AI295123	LP08661.5	825	16	1.1	751	35	AA541083	AA541083	LD08073.5	AA541083
753	16	1.1	622	87	AQ089622	AQ089622	HS_4758.A	826	16	1.1	757	69	AU080671	AU080671	AU080671	AU080671
754	16	1.1	623	48	AI589770	AI589770	tm74b08.x	827	16	1.1	767	81	B21887	B21887	F14M3-T7 IG	B21887
755	16	1.1	624	28	AA115293	AA115293	z108e10.r	828	16	1.1	767	81	B21887	B21887	F14M3-T7 IG	B21887
756	16	1.1	625	69	AW120122	AW120122	614085A07	829	16	1.1	768	40	AA979310	AA979310	LD33801.5	AA979310
757	16	1.1	625	74	AW180908	AW180908	MgA0022r	830	16	1.1	772	51	AI747711	AI747711	LD33062.5	AI747711
758	16	1.1	626	44	AI257087	AI257087	LP05352.5	831	16	1.1	795	40	AA940888	AA940888	LD33209.5	AA940888
759	16	1.1	632	44	AI295392	AI295392	LP09007.5	832	16	1.1	796	46	AI440480	AI440480	tc88g03.x	AI440480
760	16	1.1	634	47	AI486273	AI486273	EST244594	833	16	1.1	818	64	AW027041	AW027041	wt71d02.x	AW027041
761	16	1.1	634	81	B87757	B87757	RPCI11-30F1	834	16	1.1	834	45	AI360239	AI360239	qy84e08.x	AI360239
762	16	1.1	638	35	AA550252	AA550252	1374m3.qm	835	16	1.1	834	81	B01790	B01790	CSRL-140G1	B01790
763	16	1.1	638	91	AQ160965	AQ160965	nbx00006C	836	16	1.1	841	38	AA264442	AA264442	LD07769.5	AA264442
764	16	1.1	639	44	AI294628	AI294628	LP08044.5	837	16	1.1	851	82	AQ741093	AQ741093	HS_-2272.A	AQ741093
765	16	1.1	639	100	AQ279700	AQ279700	CITBI-E1-	838	16	1.1	851	82	AQ741093	AQ741093	HS_-2272.A	AQ741093
766	16	1.1	640	46	AI405479	AI405479	GH25488.5	839	16	1.1	854	51	AI762165	AI762165	ws90f07.x	AI762165
767	16	1.1	640	74	AW180930	AW180930	MgA0052r	840	16	1.1	856	82	AQ739429	AQ739429	HS_5387.B	AQ739429
768	16	1.1	642	47	AI1513498	AI1513498	GH26616.5	841	16	1.1	858	79	CNS01101	CNS01101	Drosophil	AL099660
769	16	1.1	643	30	AA202648	AA202648	LD02818.5	842	16	1.1	861	82	AQ739069	AQ739069	HS_5387.B	AQ739069
770	16	1.1	643	51	AI276042	AI276042	BNLGH1140	843	16	1.1	865	91	AQ161363	AQ161363	nbxb00006F	AQ161363
771	16	1.1	646	79	AG008123	AG008123	Homo sapi	844	16	1.1	866	91	AQ161363	AQ161363	nbxb00006F	AQ161363
772	16	1.1	647	43	AI202117	AI202117	q152b11.x	845	16	1.1	867	25	W08515	W08515	mbd47h08.r1	W08515
773	16	1.1	648	47	AI512603	AI512603	LD44522.5	846	16	1.1	884	47	AI492655	AI492655	qz18c04.x	AI492655
774	16	1.1	649	41	AI055709	AI055709	coau0004N	847	16	1.1	898	79	CNS013VU	CNS013VU	Drosophil	AL103380
775	16	1.1	651	40	AA940757	AA940757	LD22973.5	848	16	1.1	908	39	AA896283	AA896283	vx52g12.r	AA896283
776	16	1.1	651	63	AI999837	AI999837	614006C03	849	16	1.1	913	79	CNS003K7	CNS003K7	Drosophil	AL064863
777	16	1.1	652	44	AI295452	AI295452	LP09085.5	850	16	1.1	920	82	AQ688323	AQ688323	nbxb00077M	AQ688323
778	16	1.1	653	51	AI746161	AI746161	605081H04	851	16	1.1	934	69	AU079146	AU079146	AU079146	AU079146
779	16	1.1	654	61	AI833343	AI833343	605088B10	852	16	1.1	988	79	CNS006FQ	CNS006FQ	Drosophil	AL064298
780	16	1.1	656	51	AI743205	AI743205	wg98e07.x	853	16	1.1	1031	26	W41746	W41746	mc63b07.r1	W41746
781	16	1.1	658	37	AA695878	AA695878	GM04706.5	854	16	1.1	1037	79	CNS0010Z	CNS0010Z	Drosophil	AL075056
782	16	1.1	658	40	AA949140	AA949140	LD27922.5	855	16	1.1	1049	79	CNS0034E	CNS0034E	Drosophil	AL075056
783	16	1.1	663	62	AI894231	AI894231	mdl7c11.x	856	16	1.1	1101	79	CNS0003V	CNS0003V	Drosophil	AL058263
784	16	1.1	665	46	AI435832	AI435832	th79e10.x	857	16	1.1	1101	79	CNS001B0	CNS001B0	Drosophil	AL060149
785	16	1.1	667	44	AI258420	AI258420	LP01620.5	858	16	1.1	1101	79	CNS002XY	CNS002XY	Drosophil	AL064214
786	16	1.1	668	63	AW009338	AW009338	ws81b04.x	859	16	1.1	1101	79	CNS00EMU	CNS00EMU	Drosophil	AL063391
787	16	1.1	669	91	AQ157407	AQ157407	nbxb00009M	860	16	1.1	1151	80	AF094940	AF094940	Salmoneil	AF094940
788	16	1.1	670	40	AA927510	AA927510	Om70g11.s	861	16	1.1	1201	79	CNS002Z2	CNS002Z2	Drosophil	AL098312
789	16	1.1	672	69	AW108375	AW108375	um21b07.x	862	15	1.1	31	62	AI916122	AI916122	w147a09.x	AI916122
790	16	1.1	674	46	AI438586	AI438586	486012B07	863	15	1.1	55	35	AA587076	AA587076	nn77g12.s	AA587076
791	16	1.1	675	91	AQ156170	AQ156170	nbxb00002J	864	15	1.1	59	81	B44840	B44840	HS-1060-A1-	B44840
792	16	1.1	677	90	AQ047841	AQ047841	clm-3f2-t	865	15	1.1	79	34	AA525796	AA525796	n161a08.s	AA525796
793	16	1.1	677	105	AQ658119	AQ658119	Sheared.D	866	15	1.1	93	80	AF009188	AF009188	Homo sapi	AF009188
794	16	1.1	678	105	AQ641663	AQ641663	RPCI93-Dp	867	15	1.1	106	33	AA416261	AA416261	vf38f12.r	AA416261
795	16	1.1	679	102	AQ413715	AQ413715	RPCI-11-1	867	15	1.1	120	38	AA750998	AA750998	ISMJ0135	AA750998
796	16	1.1	680	100	AQ324990	AQ324990	mgxb0020M	868	15	1.1	124	30	AA219567	AA219567	zg99f10.s	AA219567
797	16	1.1	683	41	AI061971	AI061971	LD35083.5	869	15	1.1	134	32	AA371653	AA371653	EST83490	AA371653
798	16	1.1	683	105	AQ660590	AQ660590	Sheared.D	870	15	1.1	139	38	AA790379	AA790379	vw05h08.r	AA790379
799	16	1.1	684	87	AQ780297	AQ780297	HS_3169.B	871	15	1.1	140	25	N84764	N84764	J0812F Huma	N84764
800	16	1.1	687	69	AV383892	AV383892	AV383892	872	15	1.1	142	81	B22563	B22563	F15GSTR IGF	B22563
801	16	1.1	687	100	AQ274409	AQ274409	mgxb00015K	873	15	1.1	143	37	AA730270	AA730270	nz94b01.s	AA730270
802	16	1.1	688	37	AA735552	AA735552	LD21503.5	874	15	1.1	147	22	R29356	R29356	FI-477D.22	R29356
803	16	1.1	692	99	AQ200219	AQ200219	RPCI11-45	875	15	1.1	150	37	AA684852	AA684852	EST105576	AA684852
804	16	1.1	699	44	AI290794	AI290794	qml13b05.x	877	15	1.1	151	49	AI664321	AI664321	ue84e09.r	AI664321

878	15	1.1	151	60	AV128111	AV128111	AV128111	AV128111	15	1.1	235	38	AA785898	AA785898	12b06a1.f
c 879	15	1.1	152	33	AA13420	L794	Adul	AA13420	15	1.1	235	41	AI030029	AI030029	UI-R-C0-f
c 880	15	1.1	153	70	AV247421	AV247421		AV247421	15	1.1	235	70	AV241571	AV241571	AV241571
881	15	1.1	154	44	AI326950	mp39008.x		AI326950	15	1.1	235	71	AV322180	AV322180	AV322180
882	15	1.1	155	164	AV066596	AV066596		AV066596	15	1.1	236	30	AA269660	AA269660	va56f05.r
883	15	1.1	156	22	H08663	yl93a12.r1		H08663	15	1.1	236	30	AA269660	AA269660	va56f05.r
884	15	1.1	157	28	AA095518	14847.seq		AA095518	15	1.1	236	47	AI518670	AI518670	LD38312.3
c 885	15	1.1	158	62	AI929394	au59h09.y		AI929394	15	1.1	236	70	AV221640	AV221640	AV221640
c 886	15	1.1	159	72	HSNC22H05	x88272	H.sapiens D	x88272	15	1.1	236	70	AV249900	AV249900	AV249900
c 887	15	1.1	160	39	AA879783	vv98f03.r		AA879783	15	1.1	236	71	AV282691	AV282691	AV282691
888	15	1.1	161	40	AA960204	ub55b05.s		AA960204	15	1.1	237	25	N92959	N92959	zb56a11.s1
889	15	1.1	162	48	AI555056	UI-R-C2p-		AI555056	15	1.1	237	75	AV343110	AV343110	AV343110
c 890	15	1.1	163	72	AV300394	AV300394		AV300394	15	1.1	238	63	AW001620	AW001620	ws01g01.x
c 891	15	1.1	164	24	D67416	CELK052C8F		D67416	15	1.1	238	69	AW135967	AW135967	UI-H-B11-
c 892	15	1.1	165	71	AV320335	AV320335		AV320335	15	1.1	239	72	AV293029	AV293029	AV293029
c 893	15	1.1	166	59	AV078308	AV078308		AV078308	15	1.1	239	73	AV345936	AV345936	AV345936
c 894	15	1.1	167	31	AA283450	RTB218	HT	AA283450	15	1.1	240	51	AU074936	AU074936	AU074936
895	15	1.1	168	25	W18069	mb85d04.r1		W18069	15	1.1	241	30	AA259442	AA259442	va54c03.r
896	15	1.1	169	59	AV078125	AV078125		AV078125	15	1.1	241	49	AV021637	AV021637	AV021637
c 897	15	1.1	170	79	CNS000XET	AL094787	Arabidops	AL094787	15	1.1	241	50	AI696041	AI696041	tt02d10.x
898	15	1.1	171	36	AA645027	AA645027		AA645027	15	1.1	241	69	AV211114	AV211114	AV211114
c 899	15	1.1	172	73	AV360303	AV360303		AV360303	15	1.1	241	72	AV289073	AV289073	AV289073
900	15	1.1	173	49	AV004317	AV004317		AV004317	15	1.1	241	74	AV376305	AV376305	AV376305
c 901	15	1.1	174	42	AI149168	gc76a11.x		AI149168	15	1.1	243	41	AI070571	AI070571	UI-R-C2-m
c 902	15	1.1	175	48	AI546074	fb77h01.y		AI546074	15	1.1	243	51	AV057762	AV057762	AV057762
903	15	1.1	176	28	AA092435	AA092435		AA092435	15	1.1	243	73	AV351186	AV351186	AV351186
904	15	1.1	177	44	AI247243	q160d02.x		AI247243	15	1.1	244	51	AI713743	AI713743	UI-R-AG1-
c 905	15	1.1	178	47	AI464496	mv36g12.x		AI464496	15	1.1	244	62	AI931988	AI931988	614028A11
906	15	1.1	179	71	AV274950	AV274950		AV274950	15	1.1	244	70	AV247006	AV247006	AV247006
c 907	15	1.1	180	20	D35376	F00015236		D35376	15	1.1	245	20	T37102	T37102	EST102165.S
c 908	15	1.1	181	79	FR0015236	FR0015236		FR0015236	15	1.1	245	71	AV256272	AV256272	AV256272
c 909	15	1.1	182	26	W78509	W78509		W78509	15	1.1	245	72	AV331343	AV331343	AV331343
c 910	15	1.1	183	20	T57768	T57768		T57768	15	1.1	246	47	AI467479	AI467479	vd57g10.x
c 911	15	1.1	184	43	AI242891	q451e06.x		AI242891	15	1.1	246	59	AV087596	AV087596	AV087596
912	15	1.1	185	202	60	AV124957	AV124957	AV124957	15	1.1	247	48	AI612307	AI612307	486079B02
c 913	15	1.1	186	71	AV281125	AV281125		AV281125	15	1.1	247	69	AW140154	AW140154	SWAMCAC42
c 914	15	1.1	187	50	AI573389	AI573389		AI573389	15	1.1	247	71	AV267980	AV267980	AV267980
915	15	1.1	188	28	AA119443	AA119443		AA119443	15	1.1	248	25	N56054	N56054	J6470F.Huma
c 916	15	1.1	189	42	AI157834	ue59a10.r		AI157834	15	1.1	248	36	AA0606767	AA0606767	vm86e09.r
c 917	15	1.1	190	21	AA153692	tg47c08.x		AA153692	15	1.1	249	28	AA095961	AA095961	16875.seq
c 918	15	1.1	191	63	AI944423	AI944423		AI944423	15	1.1	249	51	AV055075	AV055075	AV055075
c 919	15	1.1	192	60	AV123450	AV123450		AV123450	15	1.1	249	62	AI887096	AI887096	w148a03.x
c 920	15	1.1	193	49	AV003073	AV003073		AV003073	15	1.1	249	73	AV343982	AV343982	AV343982
c 921	15	1.1	194	40	AA238425	mx92c12.r		AA238425	15	1.1	250	25	D79515	D79515	HUN274A09B
c 922	15	1.1	195	220	40	AA318855	AA318855	AA318855	15	1.1	250	43	AI232607	AI232607	EST229295
c 923	15	1.1	196	34	AA500360	AA500360		AA500360	15	1.1	250	59	AV089696	AV089696	AV089696
c 924	15	1.1	197	48	AI553692	tg47c08.x		AI553692	15	1.1	250	60	AI135645	AI135645	AV135645
925	15	1.1	198	22	AA640337	AA640337		AA640337	15	1.1	250	61	AI824453	AI824453	tx70d11.x
926	15	1.1	199	71	AV257831	AV257831		AV257831	15	1.1	250	61	AI824453	AI824453	tx70d11.x
c 927	15	1.1	200	42	AI153311	uc48c04.r		AI153311	15	1.1	250	69	AW115209	AW115209	rs62g10.y
928	15	1.1	201	61	AI845963	AI845963		AI845963	15	1.1	251	37	AA731056	AA731056	nw50g08.s
c 929	15	1.1	202	50	F19320	F19320		F19320	15	1.1	251	64	AW056440	AW056440	ST51H09.P
930	15	1.1	203	33	AA396336	AA396336		AA396336	15	1.1	251	64	AW056440	AW056440	ST51H09.P
931	15	1.1	204	61	AV175573	AV175573		AV175573	15	1.1	251	64	AW056440	AW056440	ST51H09.P
932	15	1.1	205	70	AV227465	AV227465		AV227465	15	1.1	251	64	AW056440	AW056440	ST51H09.P
c 933	15	1.1	206	102	AQ415823	AQ415823		AQ415823	15	1.1	251	64	AW056440	AW056440	ST51H09.P
c 934	15	1.1	207	40	AA991274	AA991274		AA991274	15	1.1	251	64	AW056440	AW056440	ST51H09.P
935	15	1.1	208	73	AV368200	AV368200		AV368200	15	1.1	251	64	AW056440	AW056440	ST51H09.P
c 936	15	1.1	209	34	AA503723	AA503723		AA503723	15	1.1	251	64	AW056440	AW056440	ST51H09.P
c 937	15	1.1	210	73	AV375804	AV375804		AV375804	15	1.1	251	64	AW056440	AW056440	ST51H09.P
938	15	1.1	211	50	AI707775	AI707775		AI707775	15	1.1	251	64	AW056440	AW056440	ST51H09.P
c 939	15	1.1	212	60	AV142070	AV142070		AV142070	15	1.1	251	64	AW056440	AW056440	ST51H09.P
c 940	15	1.1	213	73	AV365316	AV365316		AV365316	15	1.1	251	64	AW056440	AW056440	ST51H09.P
941	15	1.1	214	25	N60303	N60303		N60303	15	1.1	251	64	AW056440	AW056440	ST51H09.P
942	15	1.1	215	30	AV028596	AV028596		AV028596	15	1.1	251	64	AW056440	AW056440	ST51H09.P
c 943	15	1.1	216	73	AV361760	AV361760		AV361760	15	1.1	251	64	AW056440	AW056440	ST51H09.P
c 944	15	1.1	217	73	AV372182	AV372182		AV372182	15	1.1	251	64	AW056440	AW056440	ST51H09.P
945	15	1.1	218	79	FR0016825	FR0016825		FR0016825	15	1.1	251	64	AW056440	AW056440	ST51H09.P
c 946	15	1.1	219	34	AA474779	AA474779		AA474779	15	1.1	251	64	AW056440	AW056440	ST51H09.P
c 947	15	1.1	220	43	AI195386	AI195386		AI195386	15	1.1	251	64	AW056440	AW056440	ST51H09.P
948	15	1.1	221	73	AV335672	AV335672		AV335672	15	1.1	251	64	AW056440	AW056440	ST51H09.P
c 949	15	1.1	222	26	W32367	W32367		W32367	15	1.1	251	64	AW056440	AW056440	ST51H09.P
950	15	1.1	223	46	AI029083	AI029083		AI029083	15	1.1	251	64	AW056440	AW056440	ST51H09.P
c 950	15	1.1	224	59	AV113882	AV113882		AV113882	15	1.1	251	64	AW056440	AW056440	ST51H09.P

ALIGNMENTS

RESULT 1

C03492

LOCUS

DEFINITION

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

C03492 Human heart CDNA (Ynakamura) EST
30-JUL-1996
3NHC1509, mRNA sequence.
C03492 GI:1466743
human.
Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 200)
Tanaka,T., Ogiwara,A., Uchiyama,I., Takagi,T., Yazaki,Y. and
Nakamura,Y.
Construction of a normalized directionally cloned cDNA library from
adult heart and analysis of 3040 clones by partial sequencing
Genomics 35 (1), 231-235 (1996)

MEDLINE

96299762
 COMMENT On Oct 18, 1995 this sequence version replaced gi:1023268.
 Contact: Yusuke Nakamura
 Institute of Medical Science
 University of Tokyo
 4-6-1, Shirokanedai, Minato-ku, Tokyo 108, Japan
 Tel: 81-3-5449-5372
 Fax: 81-3-5449-5433
 Email: yusuke@ims.u-tokyo.ac.jp.

FEATURES

source
 1. .200
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="3NHC1609"
 /clone_lib="Human heart cDNA (Y Nakamura)"
 /dev_stage="adult"
 /note="Organ: heart; normalized directionally cloned cDNA from adult heart"
 BASE COUNT 51 a 63 c 49 g 36 t 1 others
 ORIGIN

Query Match 1.4%; Score 20; DB 27; Length 200;
 Best Local Similarity 100.0%; Pred. No. 6.4;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 817 ggcattctcttgcattccc 836
 |||||
 Db 123 GGCATCTCTTGGCATCCC 142

RESULT 2

AA958603
 LOCUS ual5e07.r1 Soares mouse mammary gland NbMMG Mus musculus cDNA clone 08-MAY-1998
 DEFINITION IMAGE:1346820 5' similar to TR:Q92743 Q92743 NOVEL SERINE PROTEASE.
 ; mRNA sequence.

ACCESSION AA958603
 VERSION AA958603.1 GI:3124833
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 304)
 AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
 TITLE The WashU-HMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT On Jan 19, 1998 this sequence version replaced gi:2282401.
 Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:695612
 Trace considered overall poor quality
 Possible reversed clone: similarity on wrong strand
 Seq primer: -28m13 rev2 ET from Amersham
 High quality sequence stop: 1.
 Location/Qualifiers
 1. 304
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:1346820"

FEATURES

source
 1. 304
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:1346820"

/clone_lib="Soares mouse mammary gland NbMMG"
 /sex="male"
 /tissue_type="mammary gland"
 /dev_stage="4 weeks"
 /lab_host="DH10B"
 /note="Organ: mammary gland; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dP) primer [5', TGTACCAATCTGAAGTGGAGCGCGCGAATGGTTTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."
 BASE COUNT 68 a 95 c 80 g 61 t
 ORIGIN

Query Match 1.4%; Score 20; DB 40; Length 304;
 Best Local Similarity 100.0%; Pred. No. 6.7;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 817 ggcattctcttgcattccc 836
 |||||
 Db 239 GGCATCTCTTGGCATCCC 258

RESULT 3

AI324092
 LOCUS mh04b12.x1 Soares mouse placenta 4NbMPL3.5 14.5 Mus musculus cDNA 23-DEC-1998
 DEFINITION clone IMAGE:441503 3' similar to TR:Q92743 Q92743 NOVEL SERINE PROTEASE. ; mRNA sequence.

ACCESSION AI324092
 VERSION AI324092.1 GI:4058521
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 329)
 AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
 TITLE The WashU-HMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT On Jan 17, 1998 this sequence version replaced gi:2044727.
 Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:266839
 This clone was previously sequenced on the 5' end only, this new data is from the 3' end
 Possible reversed clone: similarity on wrong strand
 Possible reversed clone: polyt not found
 High quality sequence stop: 325.
 Location/Qualifiers
 1. 329
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:441503"
 /clone_lib="Soares mouse placenta 4NbMPL3.5 14.5"

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 420)
AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT On Sep 12, 1996 this sequence version replaced gi:1407398.
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:360899
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 380.
Location/Qualifiers
1..420
/organism="Mus musculus"
/strain="NIH/Swiss"
/db_xref="taxon:10090"
/clone="IMAGE:586251"
/clone_lib="Stratagene mouse heart (#937316)"
/sex="pooled"
/tissue_type="heart"
/dev_stage="13 day embryos"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: heart; Vector: pBluescript SK-; Site:1:
EcorI; Site:2: XhoI; Cloned unidirectionally. Primer:
Oligo dt. 93 pooled NIH/Swiss 13 day embryo hearts.
Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5'
adaptor sequence: 5' GAATTCGCGCAGCAG 3' -3' adaptor
sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"

BASE COUNT 121 a 131 c 65 g 103 t
ORIGIN

Query Match 1.3%; Score 18; DB 29; Length 420;
Best Local Similarity 100.0%; Pred.No. 86;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1030 gacatcgctccacgctc 1047
|||||
Db 251 GACATCGCTCCACGCTC 268

Search completed: April 14, 2000, 17:43:40
Job time: 7274 sec

